



1/30

Sal I Bam H I.

----- pUC 19

Xba I

1 ATGGAGTCAA AGTTTGCTCA CATCATGTGT TTCTTTCTTC TTGCAACTTC
original sequence - ag a

51 CTTTGAAACT CTCTTGGCAC GAAAAGAAAG Tgatggacca gagatccttag
mutagenic primer

101 aacTTCAAAA GGAATTTGAA TGCAATGGAA AACAAAGGTG GCCAGAACTT

151 ATTGGTGTAC CAACAAAGCT TGCTAAGGGG ATAATTGAGA AGGAAAATTC

201 ACTCATAACT AATGTTTCTG TACTACTGAA TGGTTCTCCA GTCACAATGG

251 ATTATCGTTG TAATCGAGTT CGTCTTTTTG ATAACATTTT GGGTGATGTT

301 GTACAAATTC CTAGGGTGGC TTAA

Figure 1

1 GAATTCCGCA AGGAgcacac ccggctgtcc acctgCTGCA GAGATGGTGTC
upstream primer

51 ACGCAACCTC CCCGCTGCTG CTGCTGCTGC TGCTCAGCCT GGCTCTGGTg
cc t original sequence

101 gtccccggga tccctgcccag AAAGTGCTCG CTGACTGGGA AATGGACCAA
mutagenic primer

151 CGATCTGGGC TCCAACATGA CCATCGGGGC TGTGAACAGC AGAGGTGAAT

201 TCACAGGCAC CTACATCACA GCCGTAACAG CCACATCAAA TGAGATCAAA

251 GAGTCACCAC TGCATGGGAC ACAAACACCC ATCAACAAGA GGACCCAGCC

301 CACCTTTGGC TTCACCGTCA ATTGGAAGTT TTCAGAGTCC ACCACTGTCT

351 TCACGGGCCA GTGCTTCATA GACAGGAATG GGAAGGAGGT CCTGAAGACC

401 ATGTGGCTGC TGCGGTCAAG TGTTAATGAC ATTGGTGATG ACTGGAAAGC

451 TACCAGGGTC GGCATCAACA TCTTCACTCG CCTGCGCACA CAGAAGGAGT

501 GAGGATGGCC CCGCAAAGCC AGCAACAATG CCGGAGTGCT GACACTGCTT
↓ Hind III

551 GTGATATTCC TCCCAATAA AGCTTG

Figure 2



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EcoR I
↓
1 GAATTCGCAT ATGGCTGAAG CTGGTATCAC CGGTACTTGG TACAACCAGC
51 TGGGGTCTAC CTTTCATCGTT ACCGCTGGTG CTGACGGTGC ACTGACCGGT
101 ACTTACGAAA GCGCTGTTGG TAACGCTGAA AGCCGTTATG TTCTGACCGG
151 TCGTTACGAC TCTGCTCCGG CTACCGACGG TTCTGGTACT GCTCTGGGTT
201 GGACCGTTGC TTGGAAAAAC AACTACCGTA ACGCTCACTC TGCTACCACC
251 TGGTCTGGCC AGTACGTTGG TGGTGCTGAA GCTCGTATCA ACACCCAGTG
301 GCTGCTGACC TCTGGTACCA CCGAAGCTAA CGCTTGAAAA TCTACCCTGG
351 TTGGTCACGA CACGTTACACC AAAGTTAAAC CGTCTGCTGC TTCTATCTAG
↑
Xba I

Figure 3

Sal I altered Bam H I*

----- - pUC 19

Xba I

1 ATGGATGTTT ACAAGGAAGT TAATTTTCGTT GCTTACCTAC TAATTGTTCT
51 TGGTAAGATT TTCCTTTACT CCTTTGTTTT AAAAAATAAA AAAACAAAAA
101 AAATCTTGGT TTATACATAT ATATACACAC AAGTAGTTTT ATTTTTTTCC
151 TTTATATTAT ATTGTTGTA GGAATATTTT TACTTGTTAG CGTGGTGGA
201 CATGTTGATG CGAAGATCTG TACTAAAGAA TGTGGTAATC TTGGGTTTGG
251 GATATGCCCA CGTTCAGAAG GAAGTCCGAA AAATCCCATAT TGCATCAATT
301 GTTGCTCAGG CTATAAGGGT TGTAATTATT ATAGTGTTTT CGGGAGATTT
351 ATTTGCGAAG GAGAATCTGA CCTAAAAAAC CCAAAGCTT GCCCCCTAAA
401 TTGTGATACA AATATTGCCT ATTCAAGATG CCCCATTCA GAAGGAAAAT
451 CGCTAATTTA TCCCACCGGA TGTACCACAT GTTGACACAGG GTACAAGGGT
501 TGCTACTATT TCGGTAAAAA TGGCAAGTTT GTATGCGAAG GAGAGAGTGA
551 TGAACCCAAG GCAAATATGT ACCCTGCAAT GTGA

* result of PCR error during isolation of the PPI-II sequence

Figure 4





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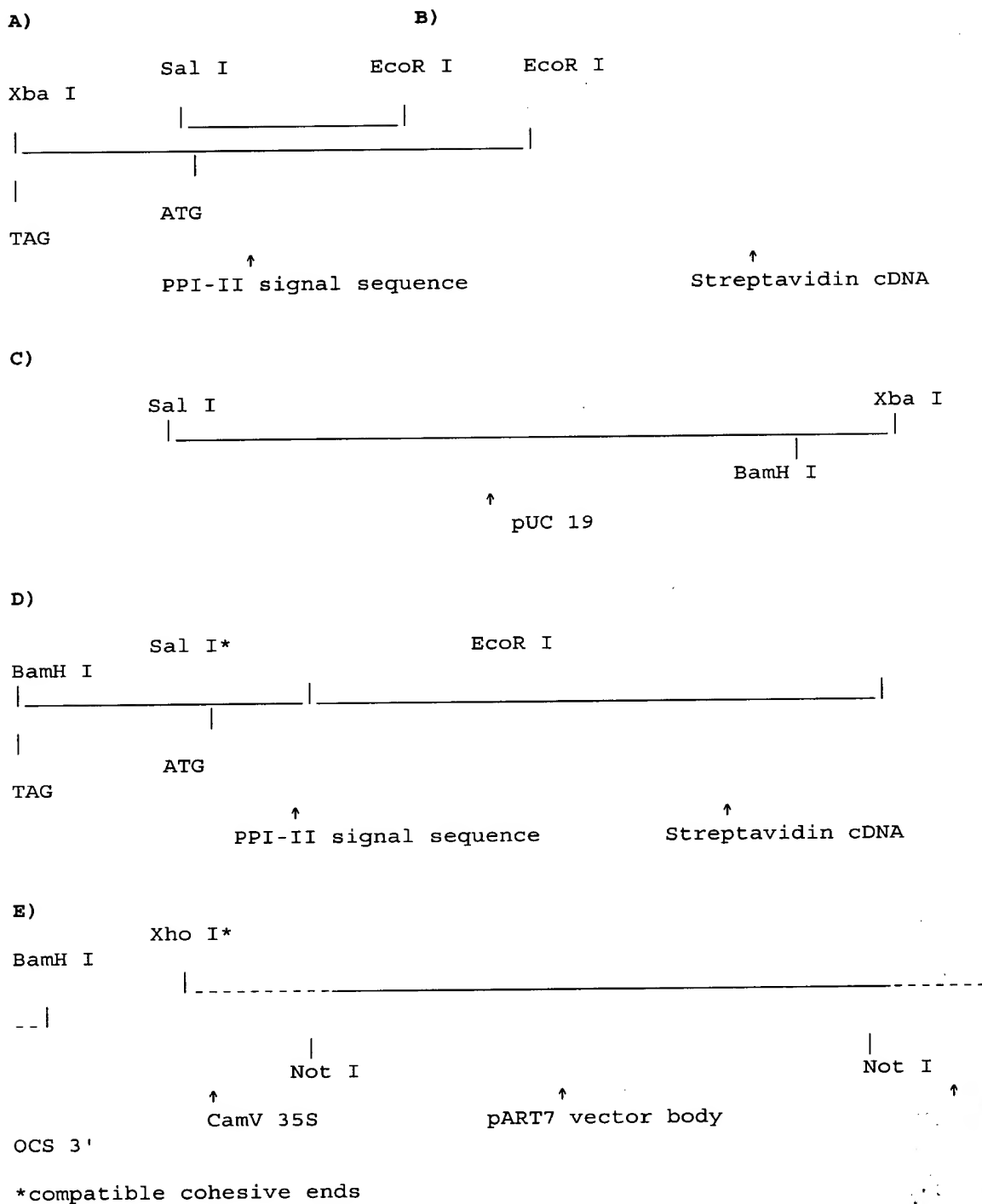


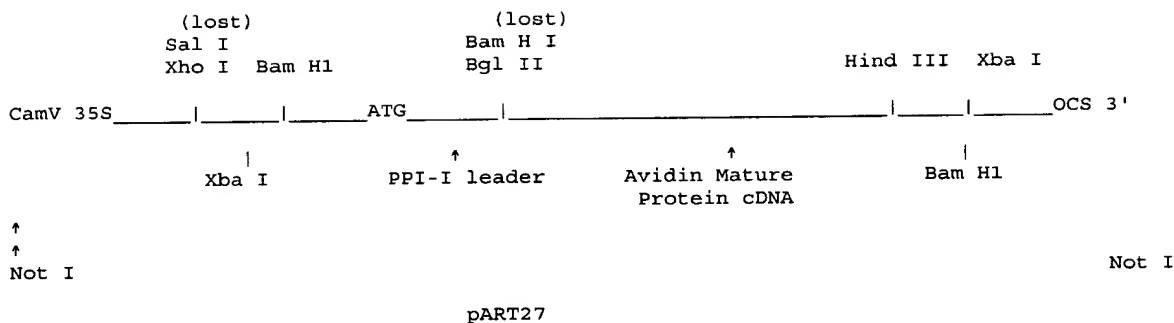
Figure 6



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A)



B)

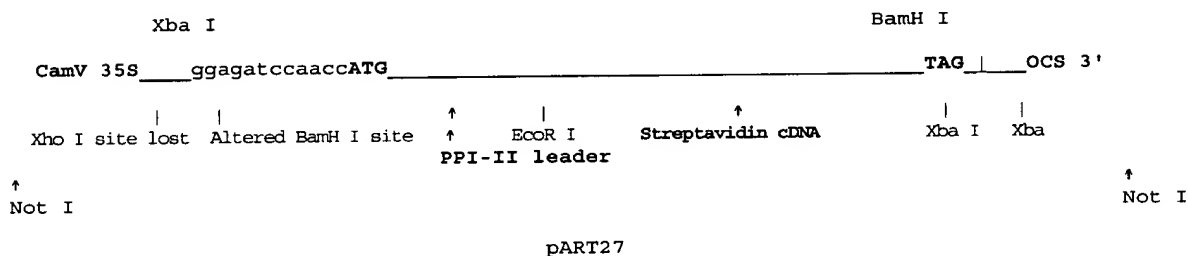


Figure 7

A)

1 ATGGAGTCAA AGTTTGCTCA CATCATTGTT TTCTTTCTTC TTGCAACTCC

51 CTTTGAAACT CTCTTGGCAC GAAAAGAAAG TGATGGACCA GAGATCCCTG

101 CCAGAAAGTG CTCGCTGACT GGGAAATGGA CCAACGATCT GGGCTCCAAC

151 ATGACCATCG GGGCTGTGAA CAGCAGAGGT GAATTCACAG GCACCTACAT

201 CACAGCCGTA ACAGCCACAT CAAATGAGAT CAAAGAGTCA CCATTGCATG

251 GGACACAAAA CACCATCAAC AAGAGGACCC AGCCACCTT TGGCTTCACC

301 GTCAATTGGA AGTTTTTCAGA GTCCACCACT GTCTTCACGG GCCAGTGCTT

351 CATAGACAGG AATGGGAAGG AGGTCCTGAA GACCATGTGG CTGCTGCGGT

401 CAAGTGTTAA TGACATTGGT GATGACTGGA AAGCTACCAG GGTCCGGCATC

451 AACATCTTCA CTCGCCTGCG CACACAGAAG GAGTGA

B)

cleavage site

1 MESKFAHIIV FFLLATPFET LLARKESDGP EipARKCSLT GKWTNDLGSN

51 MTIGAVNSRG EFTGTYITAV TATSNEIKES PLHGTQNTIN KRTQPTFGFT

101 VNWKFSESTT VFTGQCfidr NGKEVLKTMW LLRSSVNDIG DDWKATRVGI

151 NIFTRLRTQK E*

Figure 8





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A)

1 ATGGATGTTT ACAAGGAAGT TAATTTTCGTT GCTTACCTAC TAATTGTTCT
51 TGGTAAGATT TTCCTTTACT CCTTTGTTTT AAAAAATAAA AAAACAAAAA
101 AAATCTTGGT TTATACATAT ATATACACAC AAGTAGTTTT ATTTTTTTCC
151 TTTATATTAT ATTTGTTGTA GGAATATTTT TACTTGTTAG CGTGGTGGAA
201 CATGTTGATG CGAAGATCTG TACTAAGAAT TCGCATATGG CTGAAGCTGG
251 TATCACCGGT ACTTGGTACA ACCAGCTGGG GTCTACCTTC ATCGTTACCG
301 CTGGTGCTGA CGGTGCACTG ACCGGTACTT ACGAAAGCGC TGTTGGTAAC
351 GCTGAAAGCC GTTATGTTCT GACCGGTCGT TACGACTCTG CTCCGGCTAC
401 CGACGGTTCT GGTACTGCTC TGGGTTGGAC CGTTGCTTGG AAAACAACCT
451 ACCGTAACGC TCACTCTGCT ACCACCTGGT CTGGCCAGTA CGTTGGTGGT
501 GCTGAAGCTC GTATCAACAC CCAGTGGCTG CTGACCTCTG GTACCACCGA
551 AGCTAACGCT TGGAAATCTA CCCTGGTTGG TCACNACACG TTCACCAAAG
601 TTAAACCGTC TGCTGCTTCT ATCTAG

B)

cleavage site



1 MDVHKEVNFV AYLLIVLGIF LLVSVVEHVD AKICTKnshM AEAGITGTWY
51 NQLGSTFIVT AGADGALTGT YESAVGNAES RYVLTGRYDS APATDGSGTA
101 LGWTVAWKNN YRNAHSATTW SGQYVGAEAE RINTQWLLTS GTTEANAWKS
151 TLVGHDTFTK VKPSAASI*

Figure 9



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September 1997

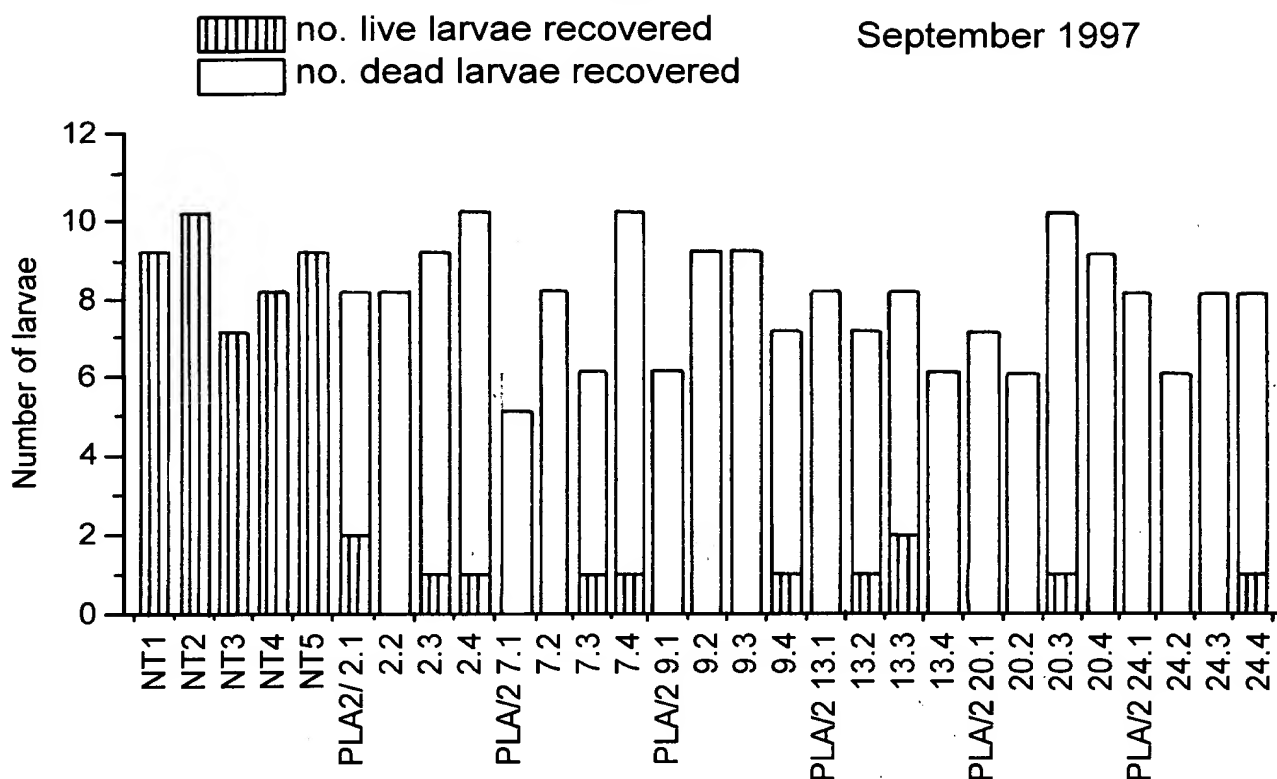


FIG. 10

October 1997

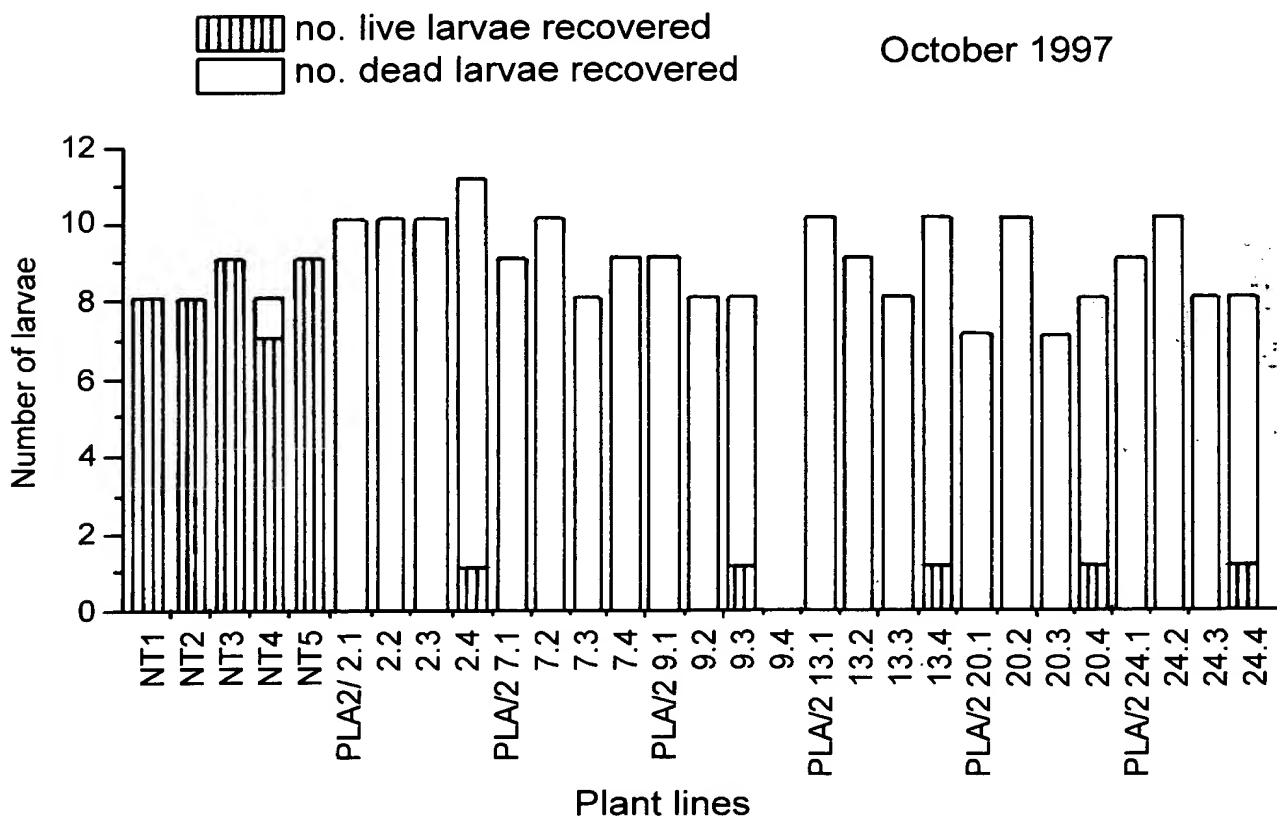


FIG. 11



A)

1 CCCTCCGTCC CCGCCGGGCA ACAACTAGGG AGTATTTTTC GTGTCTCACA
51 TGGCGAAGAT CGTCGTTGCA GCCATCGCCG TTTCCCTGAC CACGGTCTCG
101 ATTACGGCCA GCGCTTCGGC AGACCCCTCC AAGGACTCGA AGGCCCAGGT
151 CTCGGCCGCC GAGGCCGGCA TCACCGGCAC CTGGTACAAC CAGCTCGGCT
201 CGACCTTCAT CGTGACCGCG GCGCCCGACG GCGCCCTGAC CGGAACCTAC
251 GAGTCGGCCG TCGGCAACGC CGAGAGCCGC TACGTCCTGA CCGGTCGTTA
301 CGACAGCGCC CCGGCCACCG ACGGCAGCGG CACCGCCCTC GGTGAGACGG
351 TGGCCTGGAA GAATAACTAC CGCAACGCCC ACTCCGCGAC CACGTGGAGC
401 GGCCAGTACG TCGGCGGCGC CGAGGCGAGG ATCAACACCC AGTGGCTGCT
451 GACCTCCGGC ACCACCGAGG CCAACGCCTG GAAGTCCACG CTGGTCGGCC
501 ACGACACCTT CACCAAGGTG AAGCCGTCCG CCGCCTCCAT CGACGCGGCG
551 AAGAAGGCCG GCGTCAACAA CGGCAACCCG CTCGACGCCG TTCAGCAGTA
601 GTCGCGTCCC GGCACCGGCG GGTGCCGGA CCTCGGCC

B)

1 MRKIVVAAIA VSLTTVSITA SASADPSKDS KAQVSAEAG ITGTWYNQLG
51 STFIVTAGAD GALTGTYESA VGNAESRYVL TGRYDSAPAT DSGGTALGWT
101 VAWKNNYRNA HSATTWSGQY VGGAEARINT QWLLTSGTTE ANAWKSTLVG
151 HDTFTKVKPS AASIDAAKKA GVNNGNPLDA VQQ

Figure 12



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Figure 13

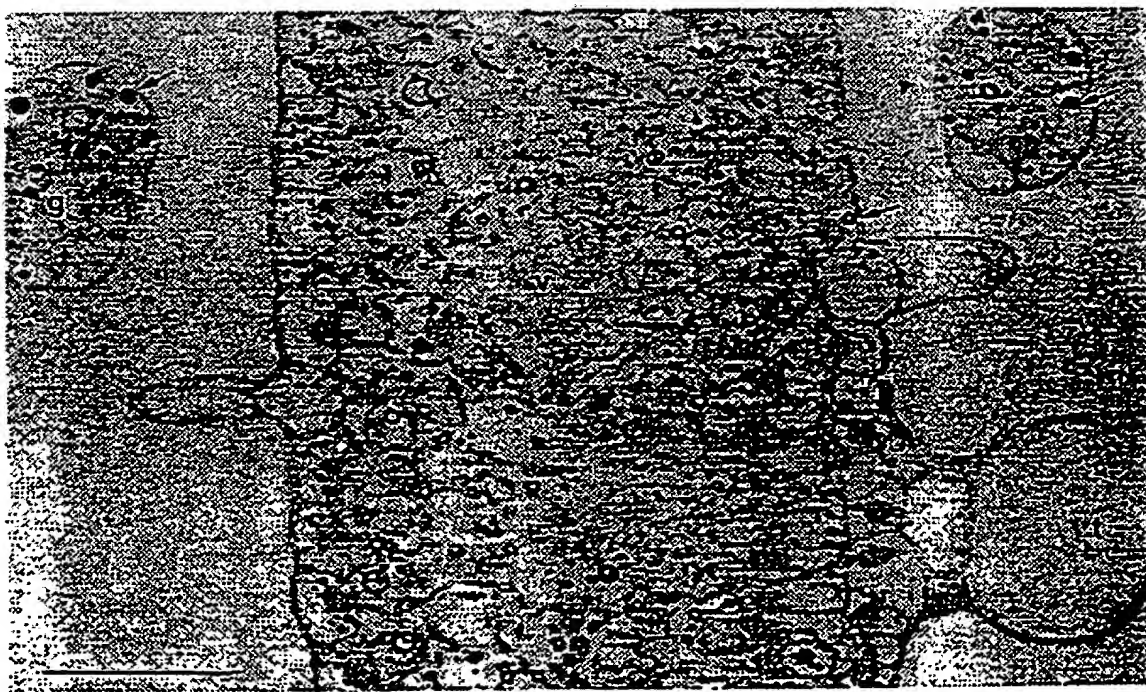


Figure 14

2003-05-23 10:00:00



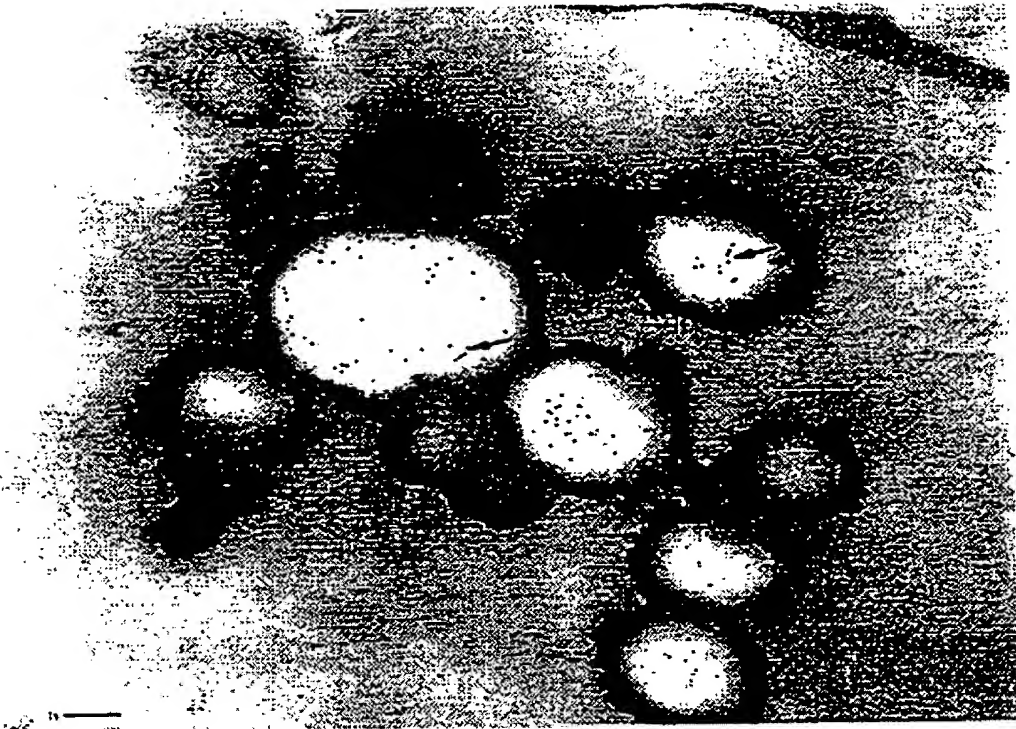


Figure 15



Figure 16

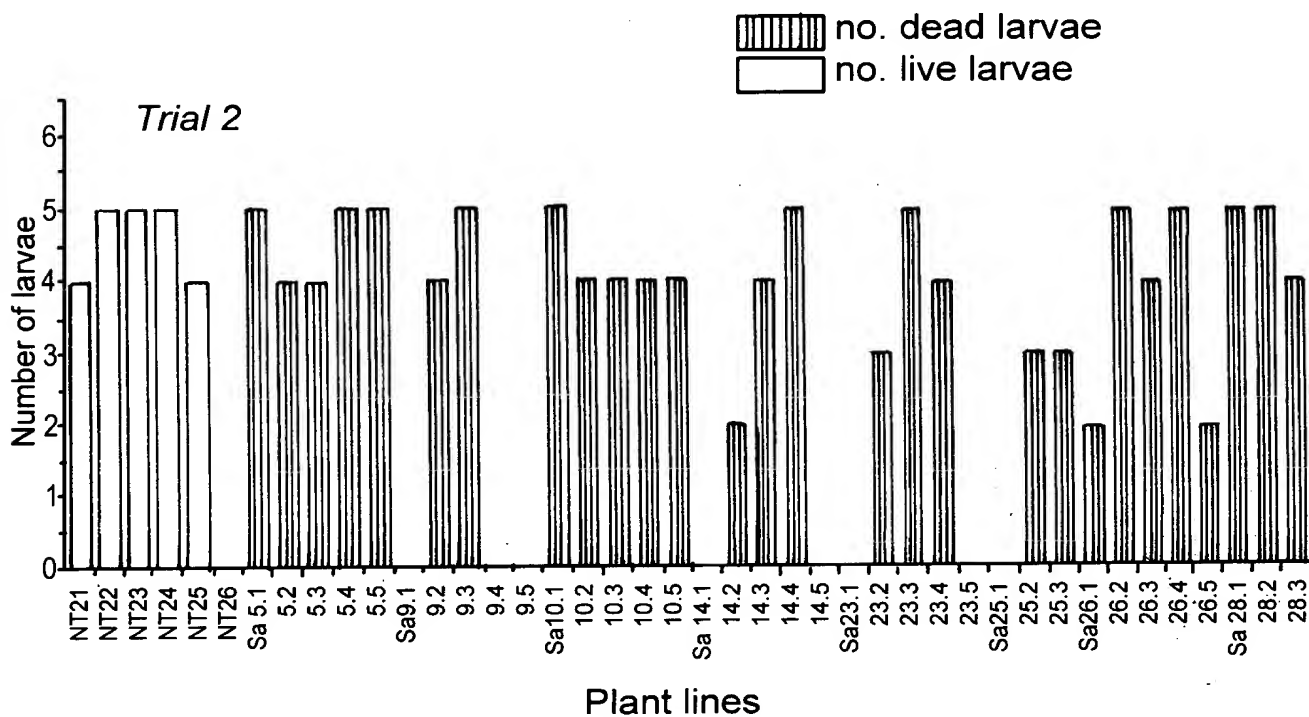
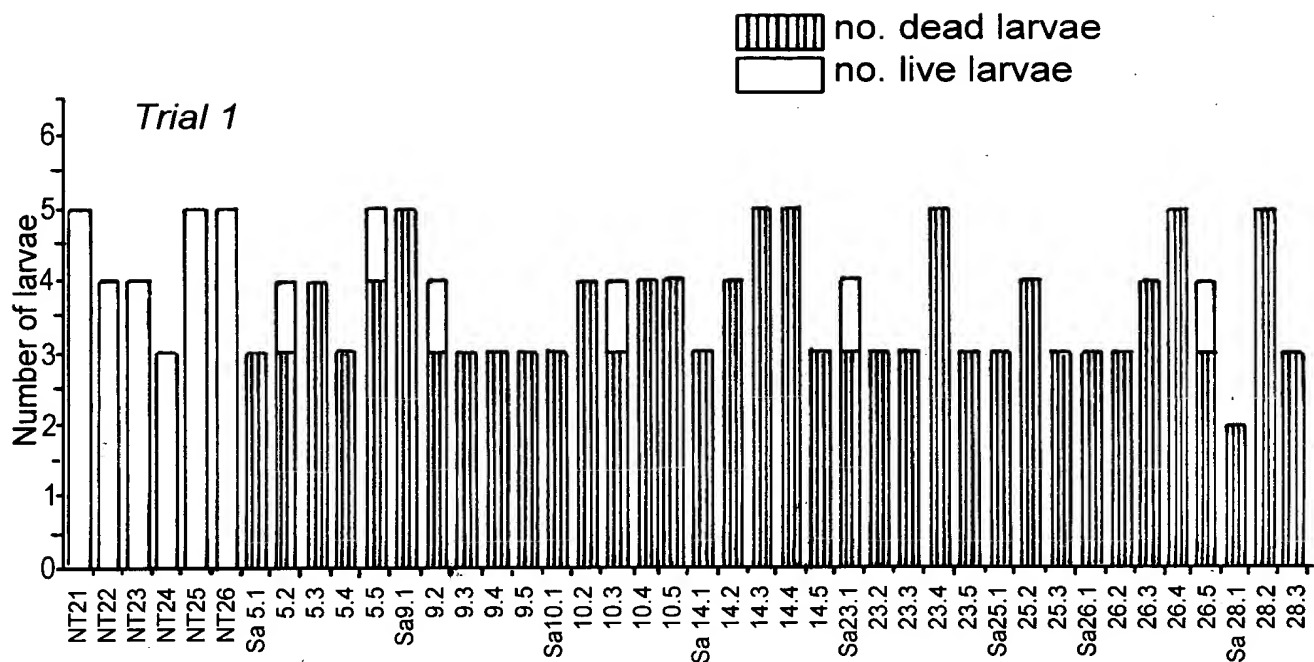


FIG. 17

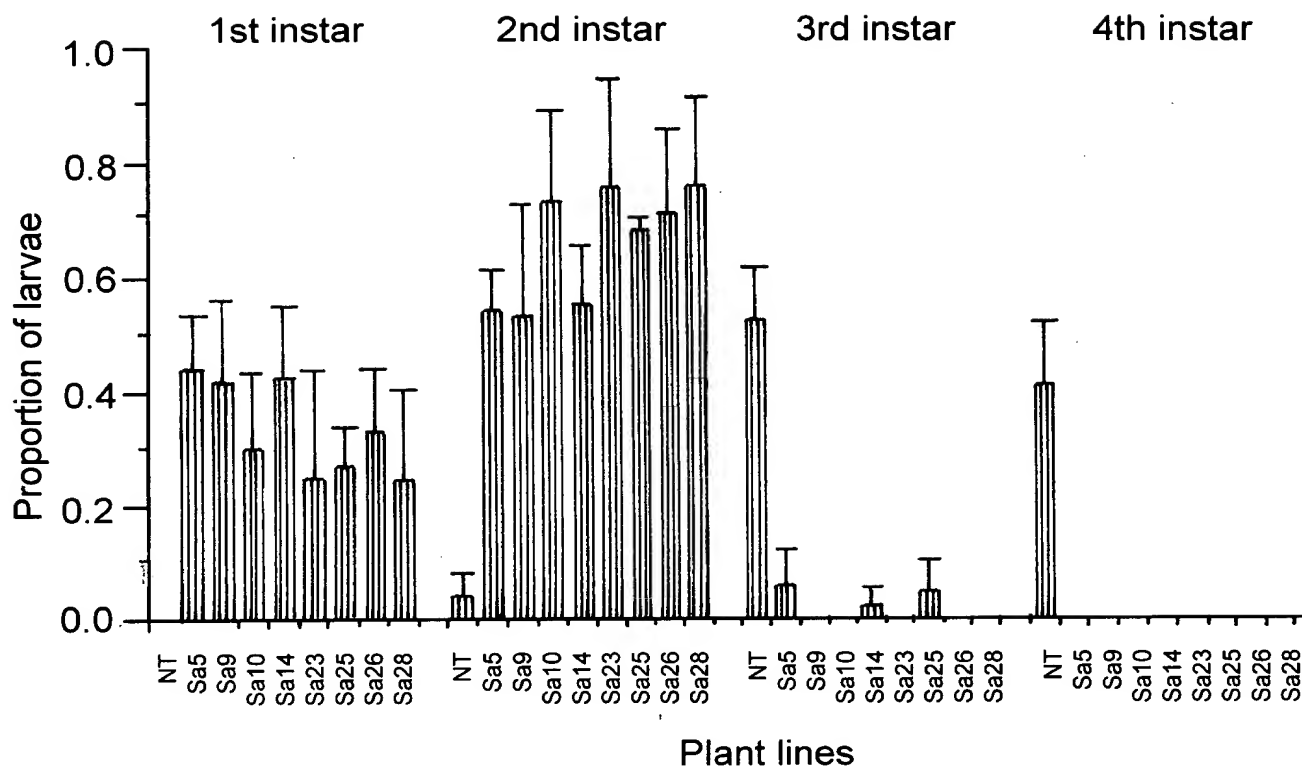


FIG. 18

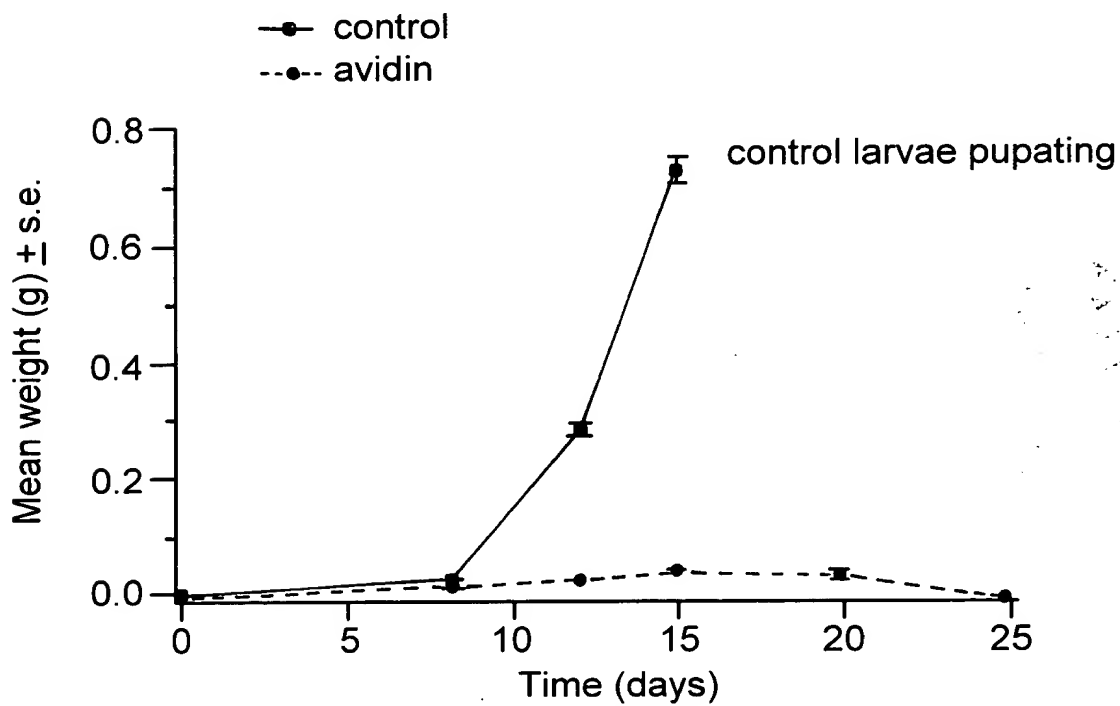


FIG. 19A

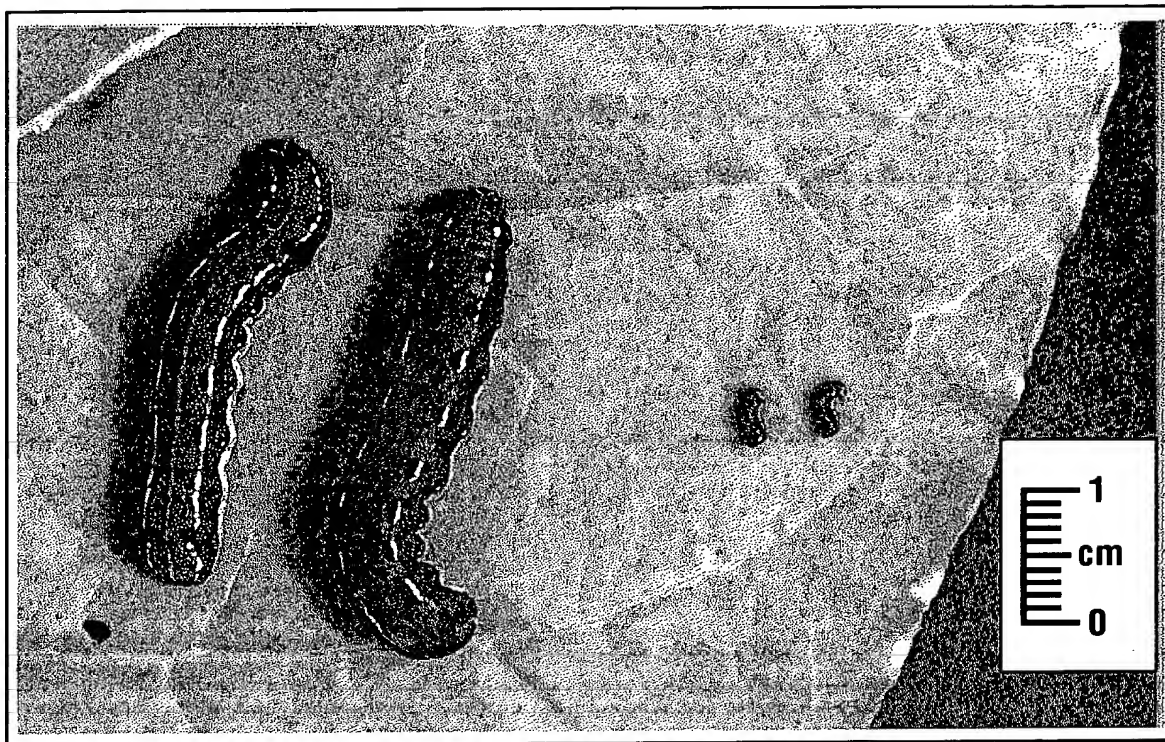


Figure 19B



Figure 19C



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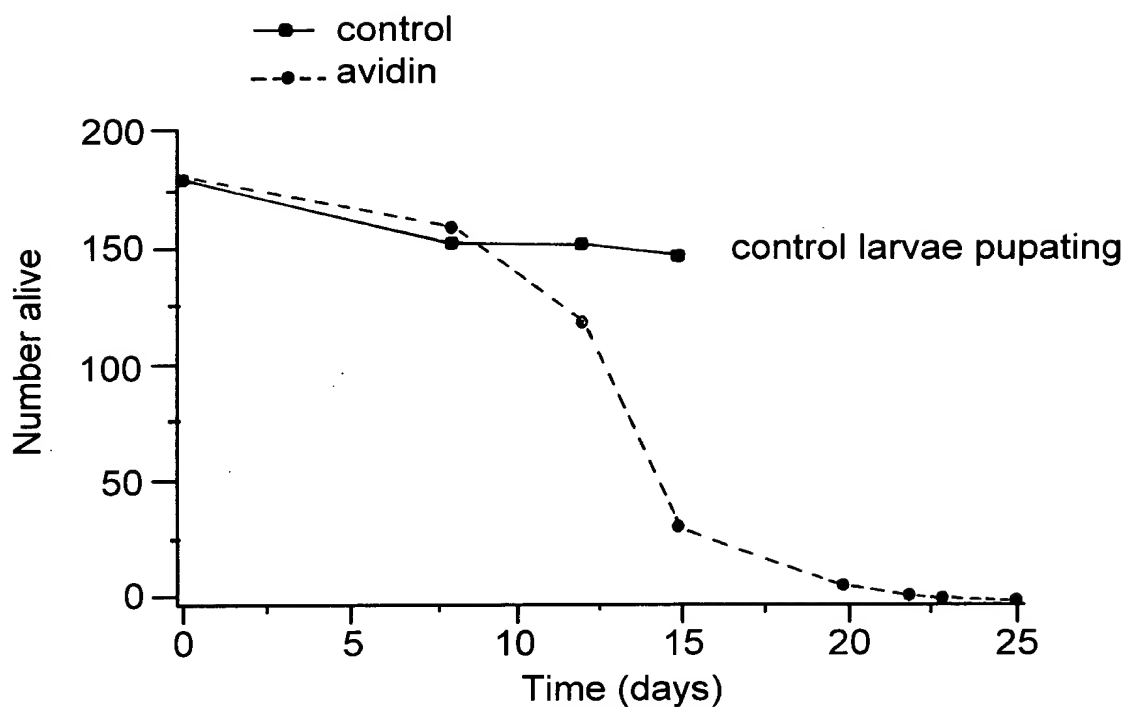


FIG. 20

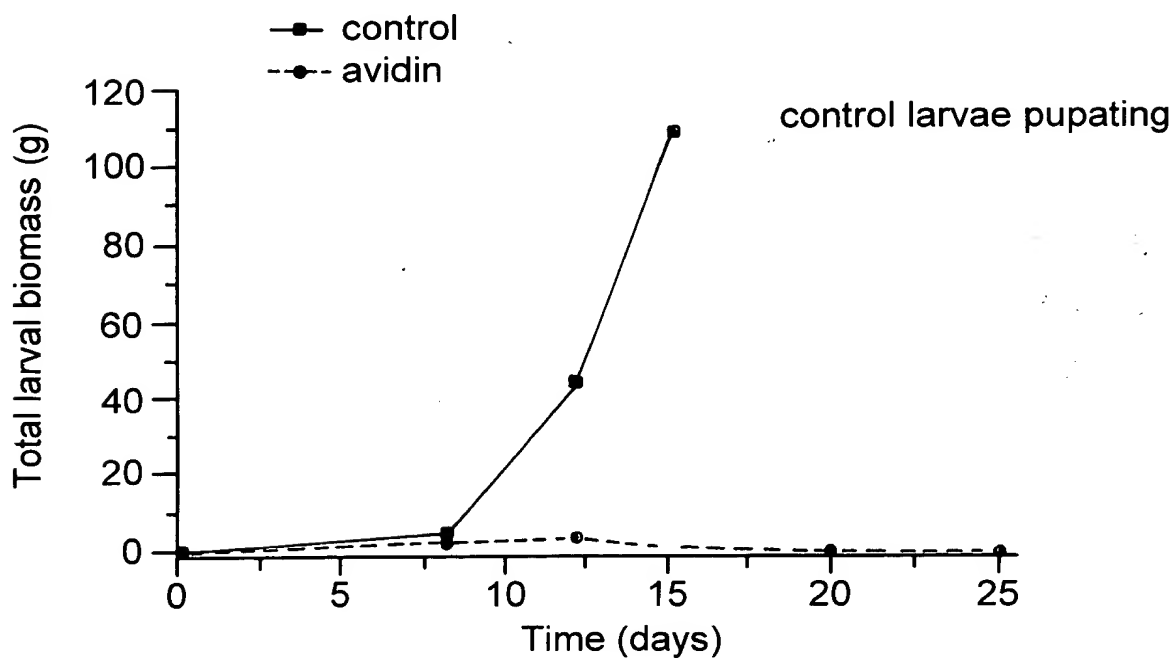


FIG. 21



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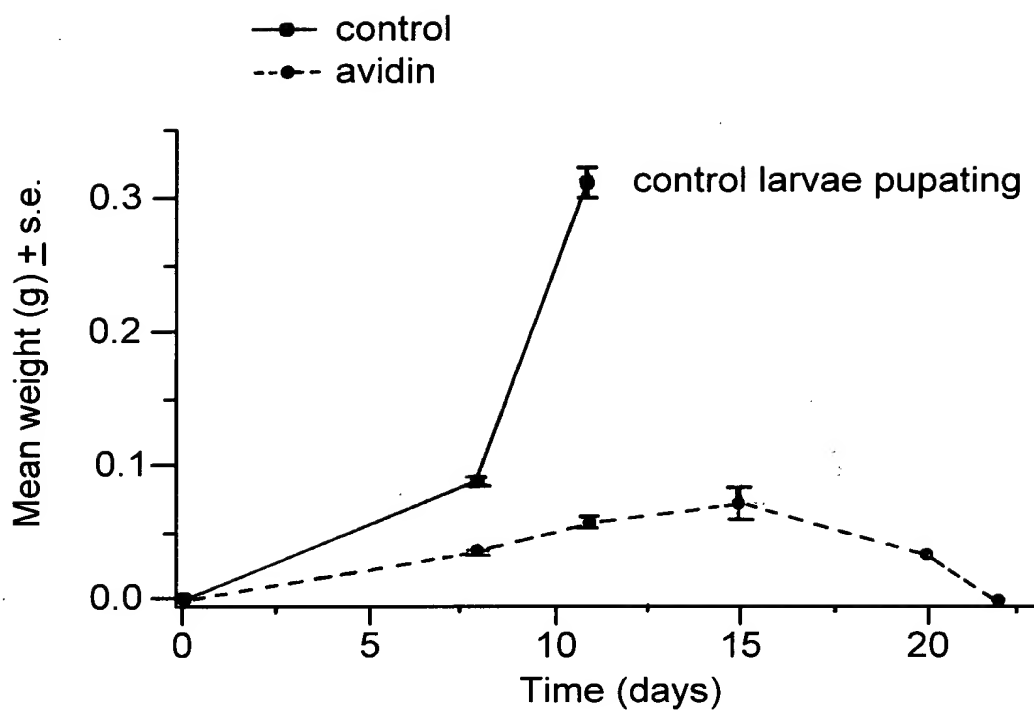


FIG. 22A

+

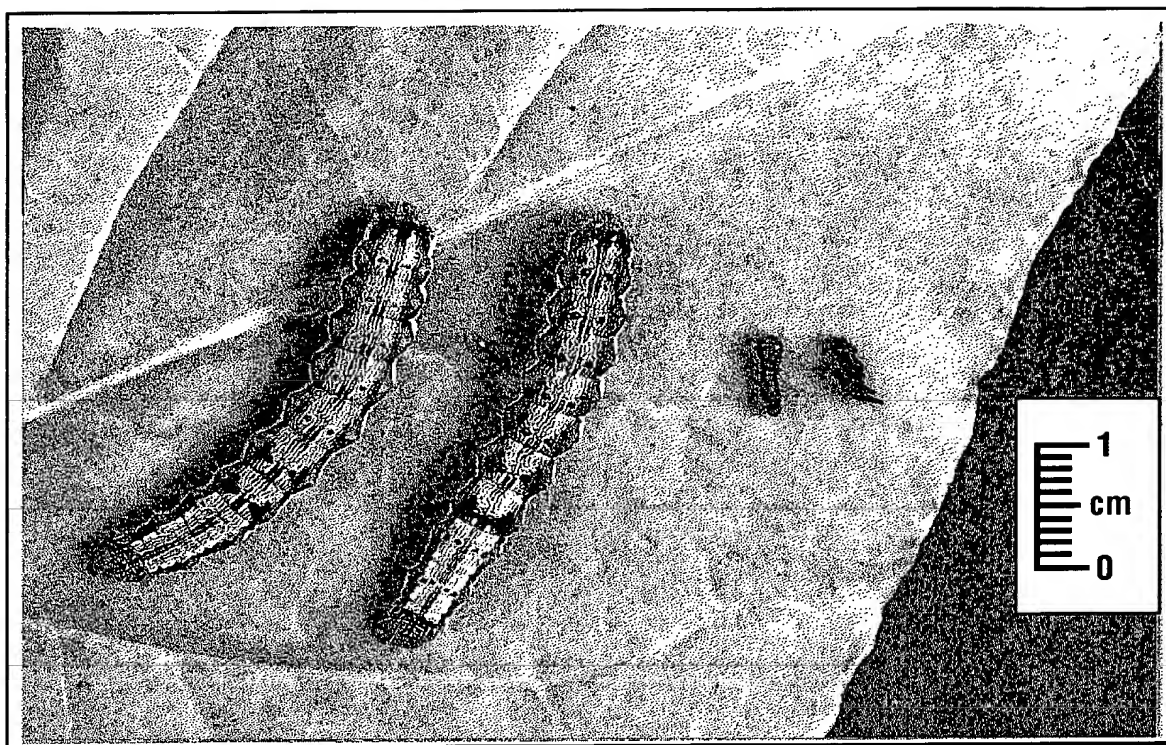


Figure 22B



Figure 22C



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+

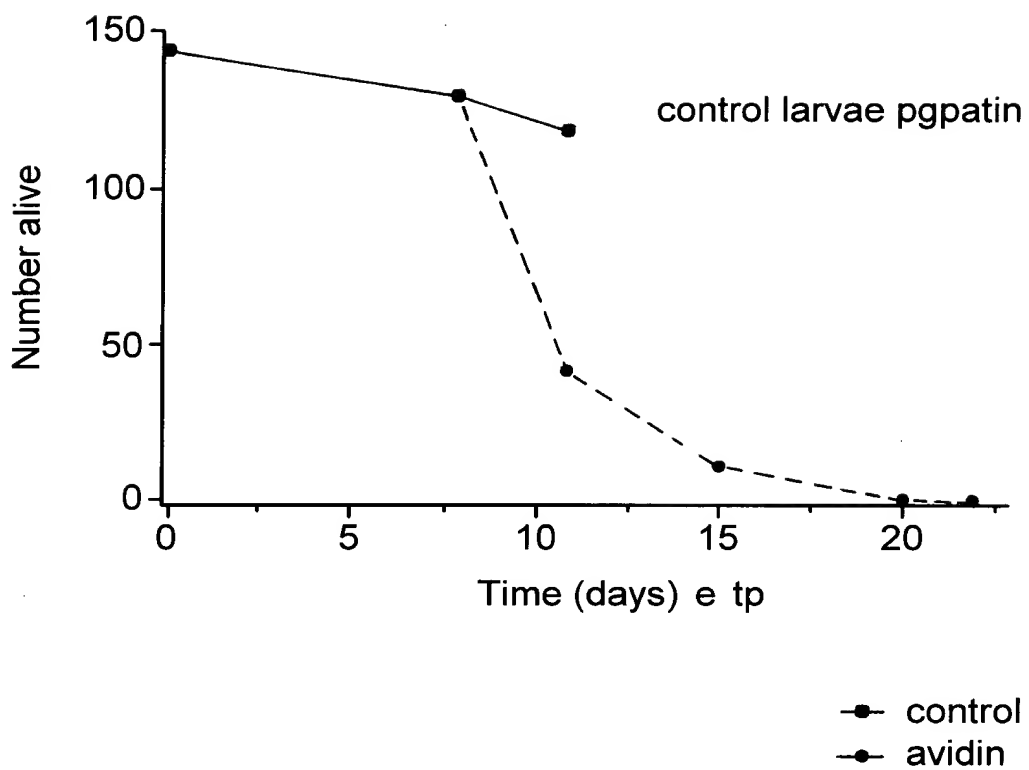


FIG. 23

+

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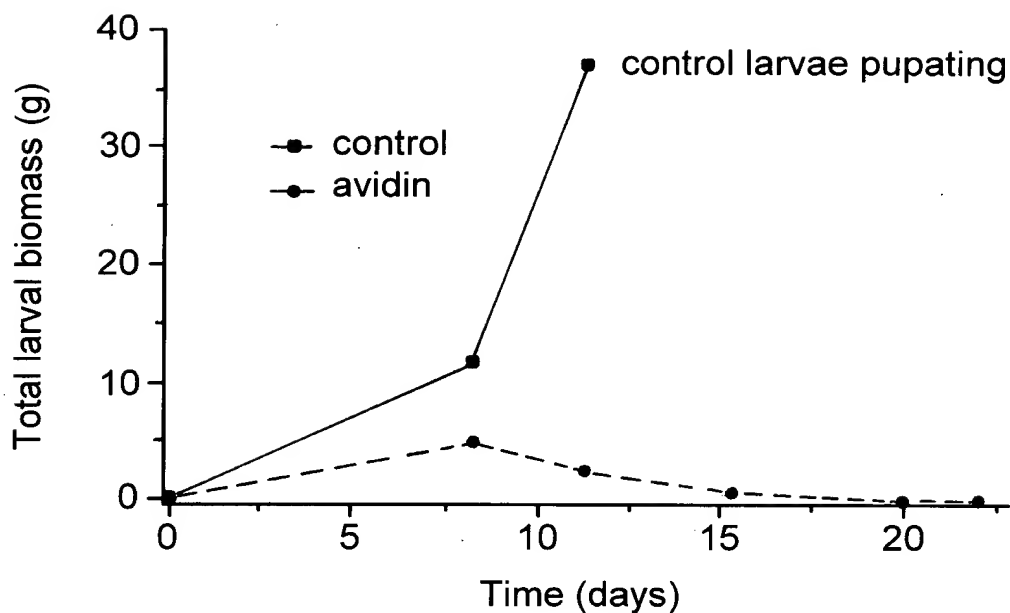


FIG. 24

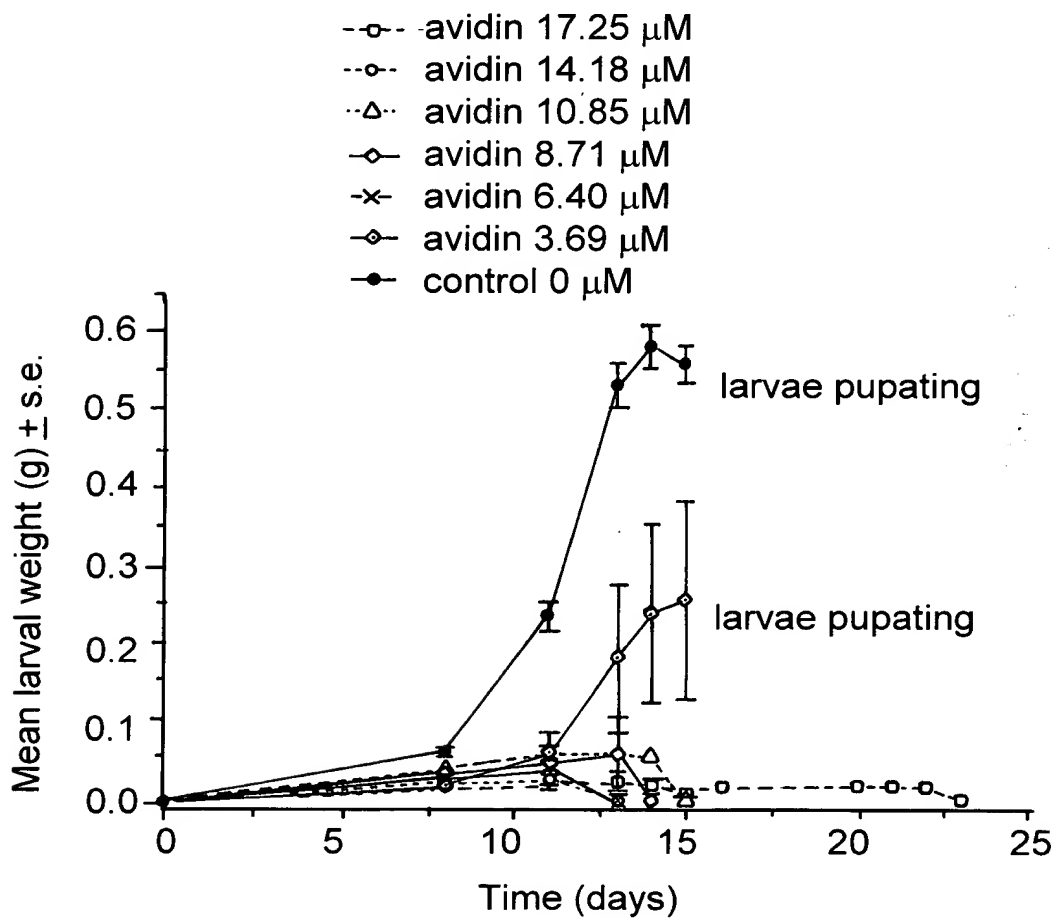


FIG. 25

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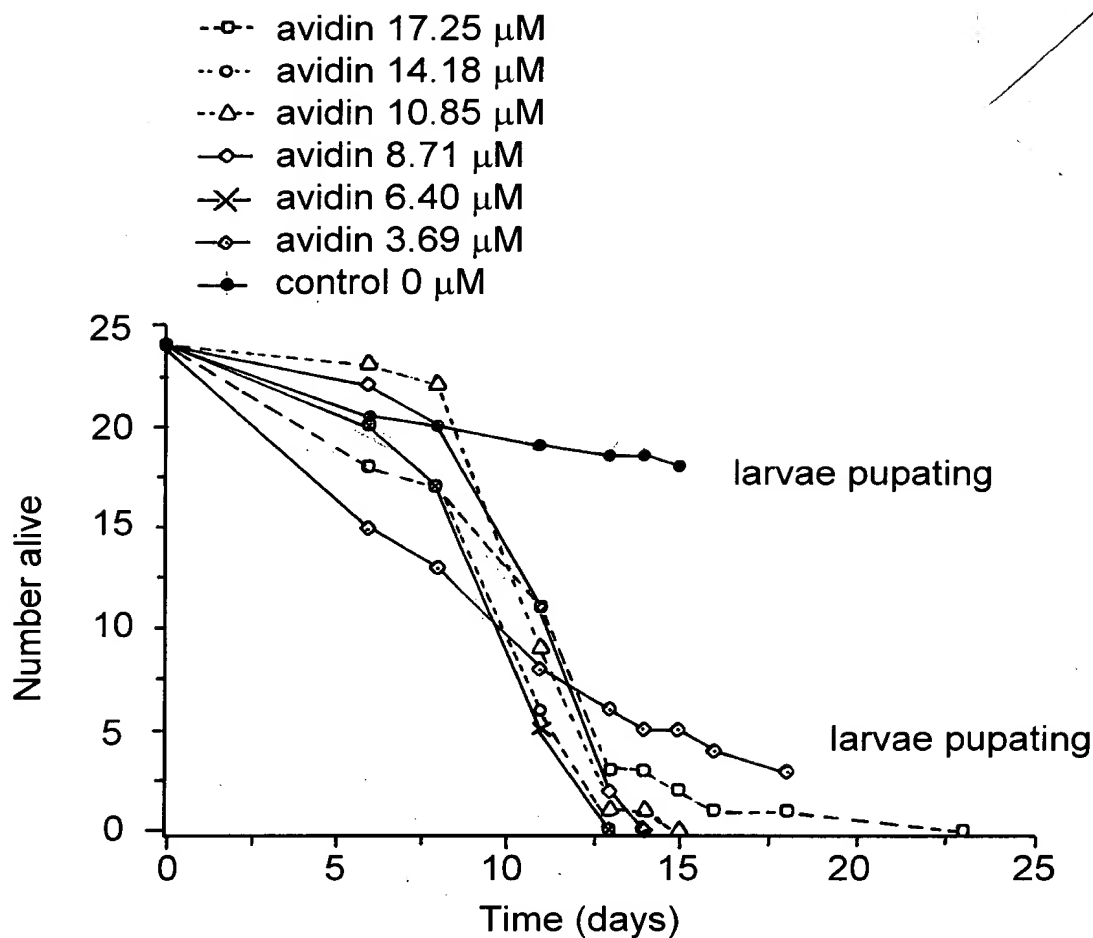


FIG. 26

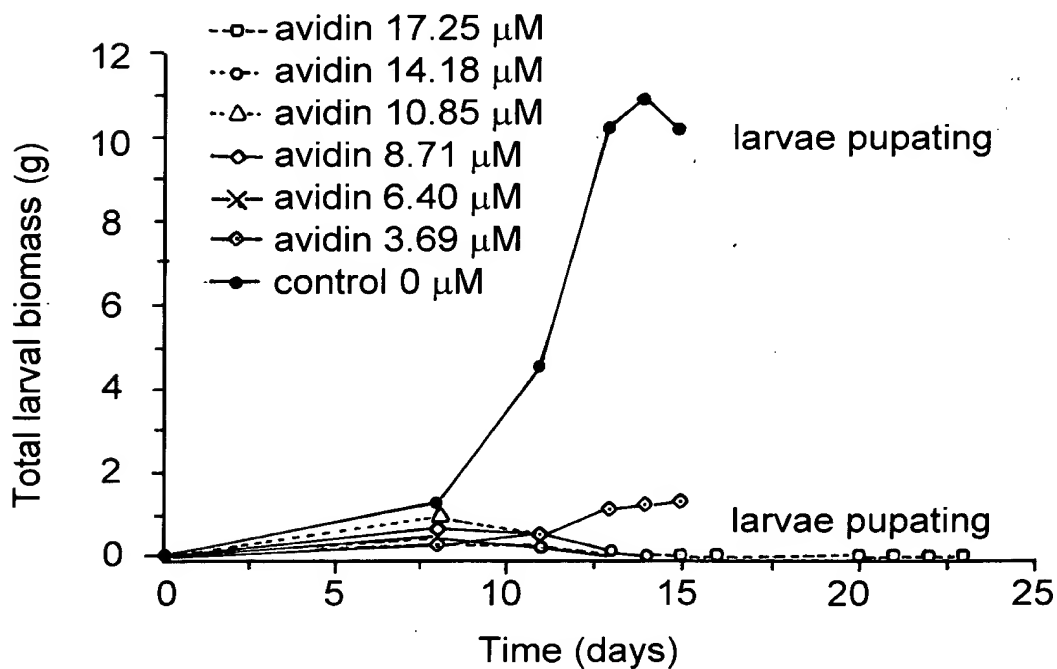


FIG. 27

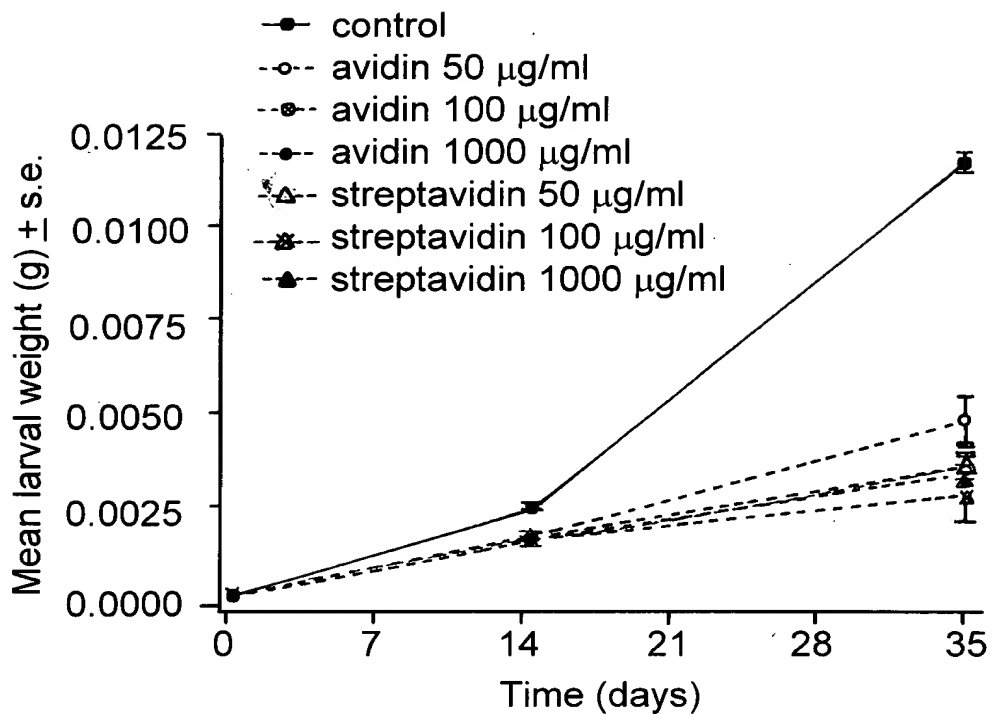


FIG. 28

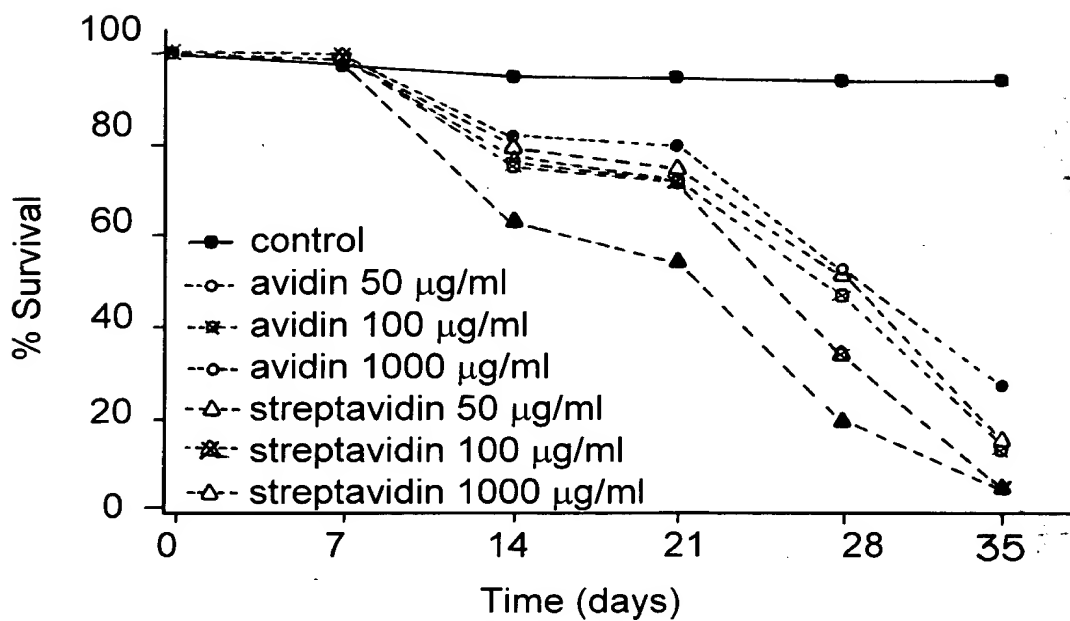


FIG. 29



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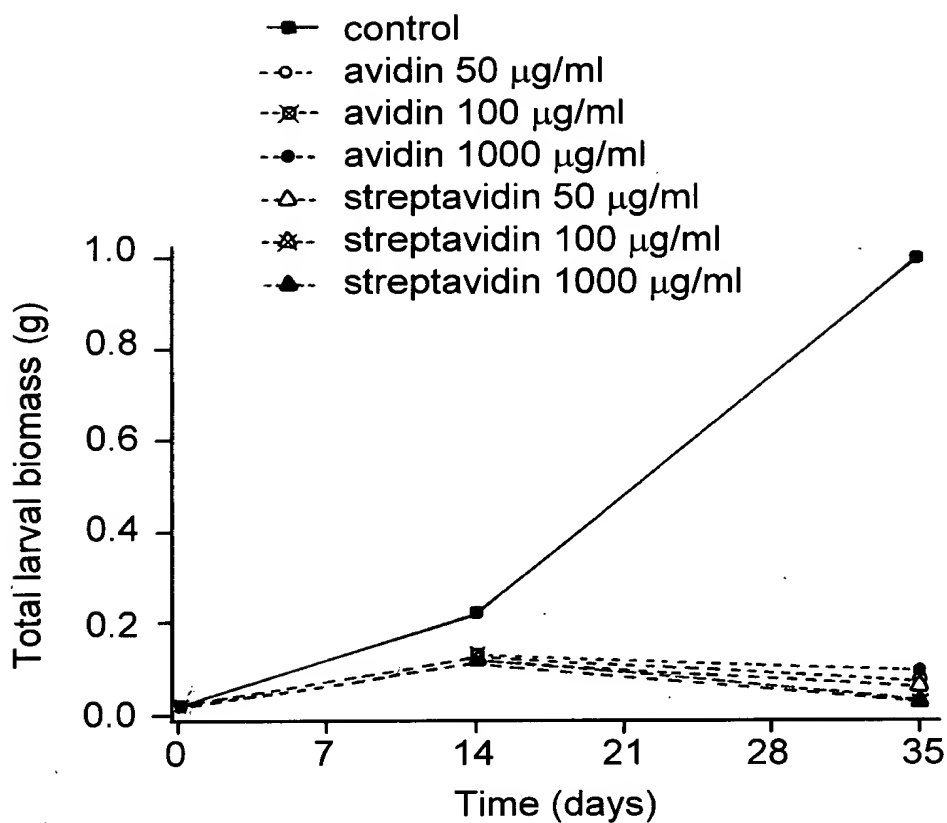


FIG. 30

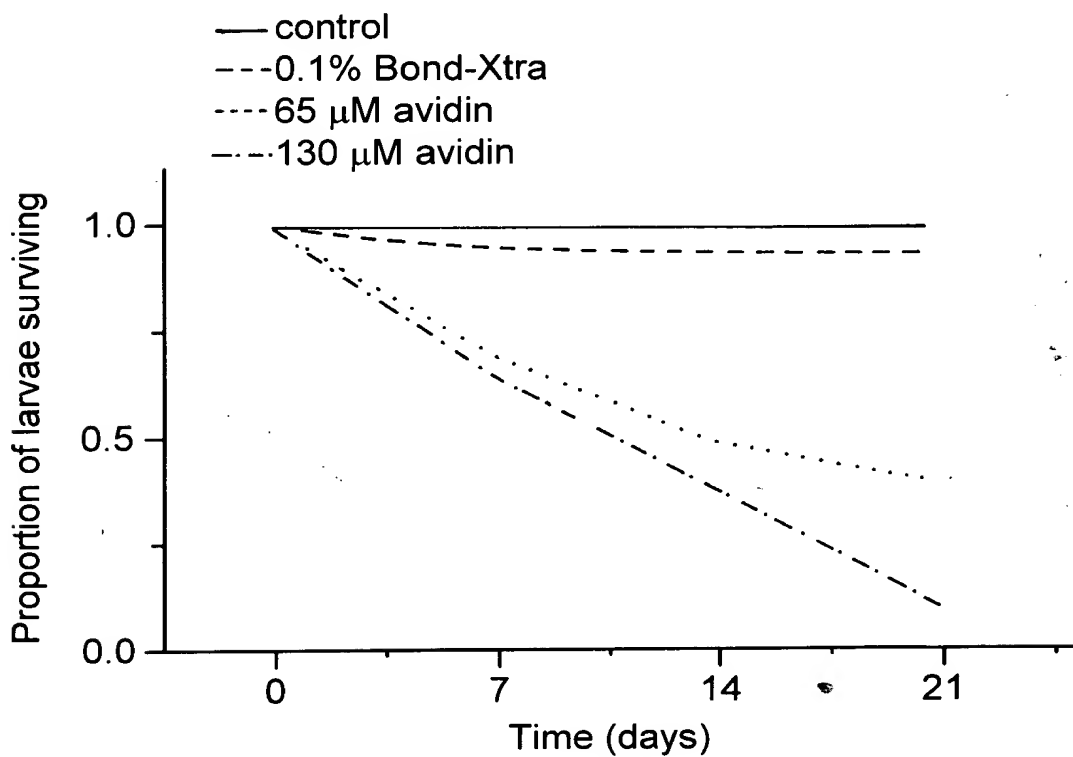


FIG. 31

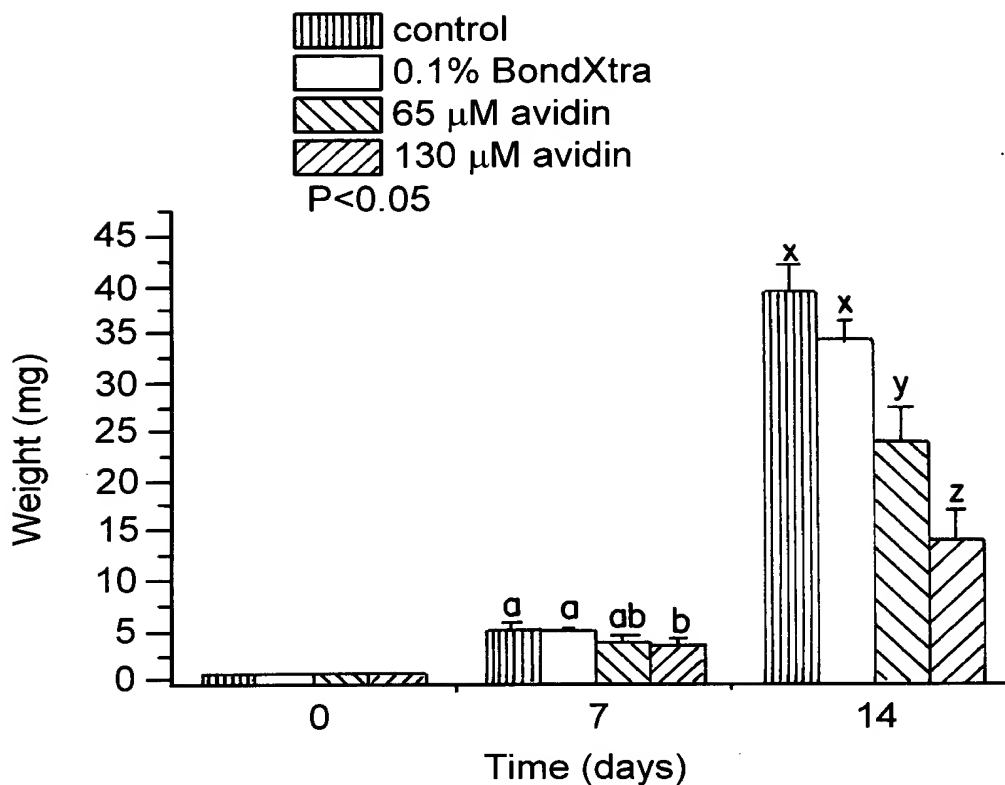


FIG. 32

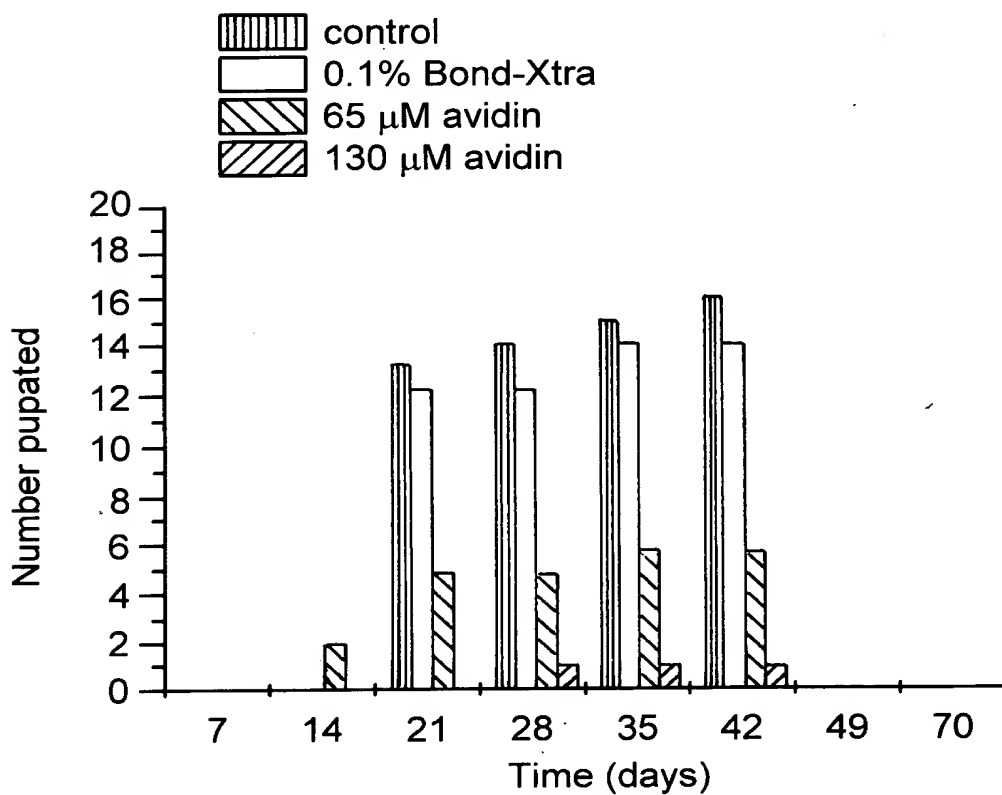


FIG. 33

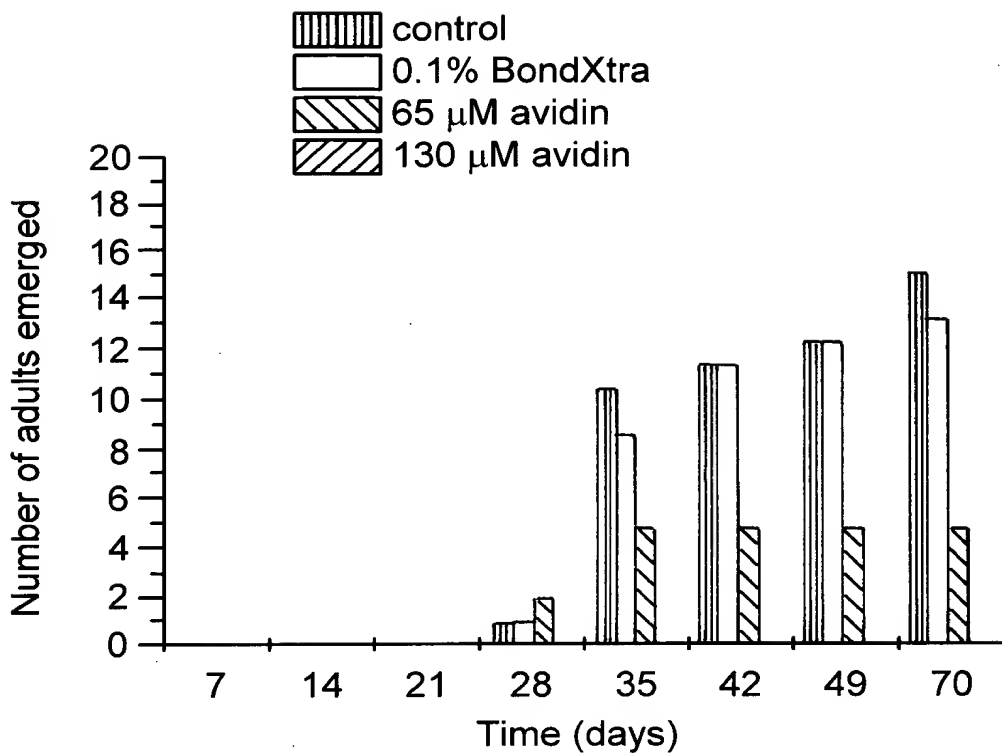


FIG. 34

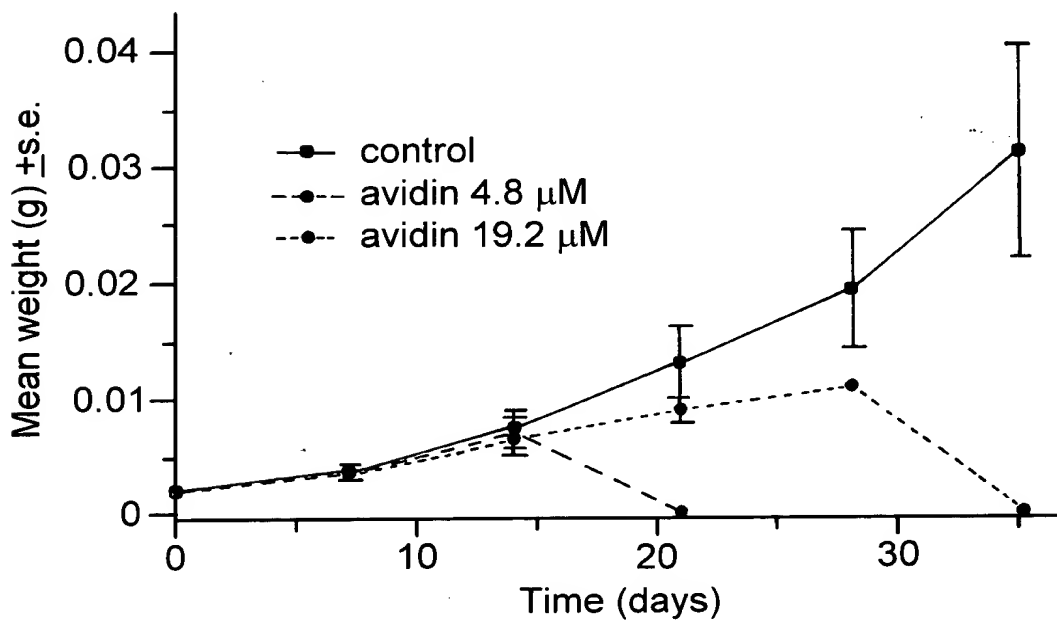


FIG. 35

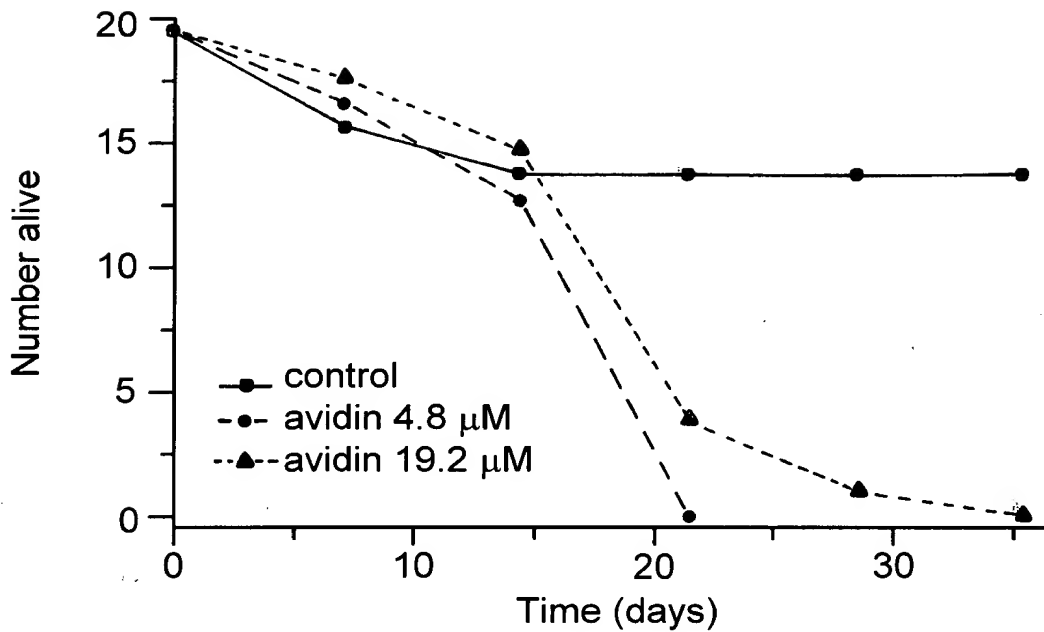


FIG. 36

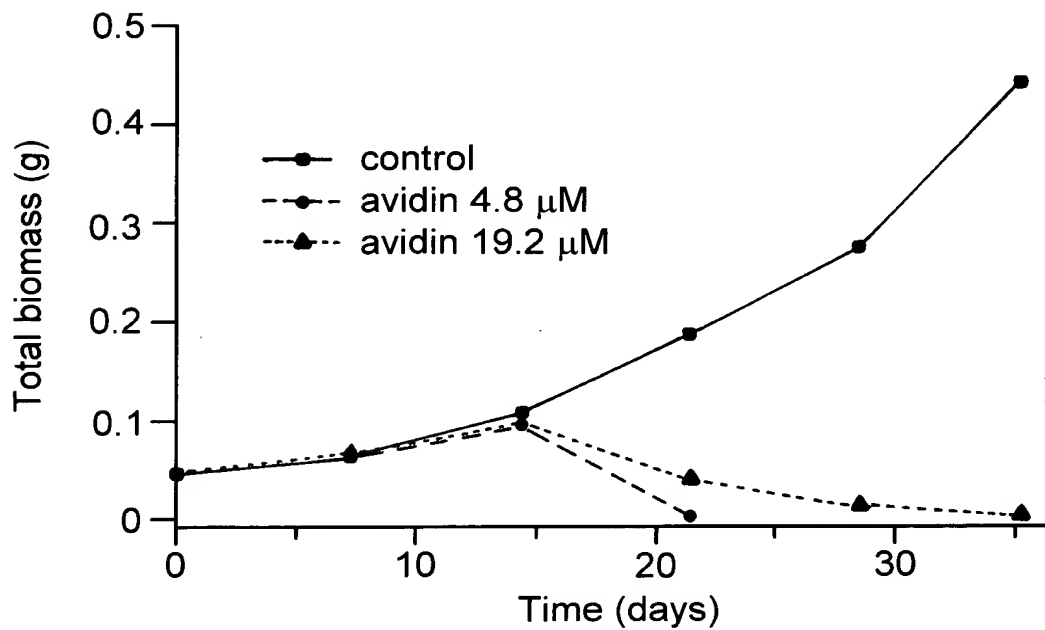


FIG. 37

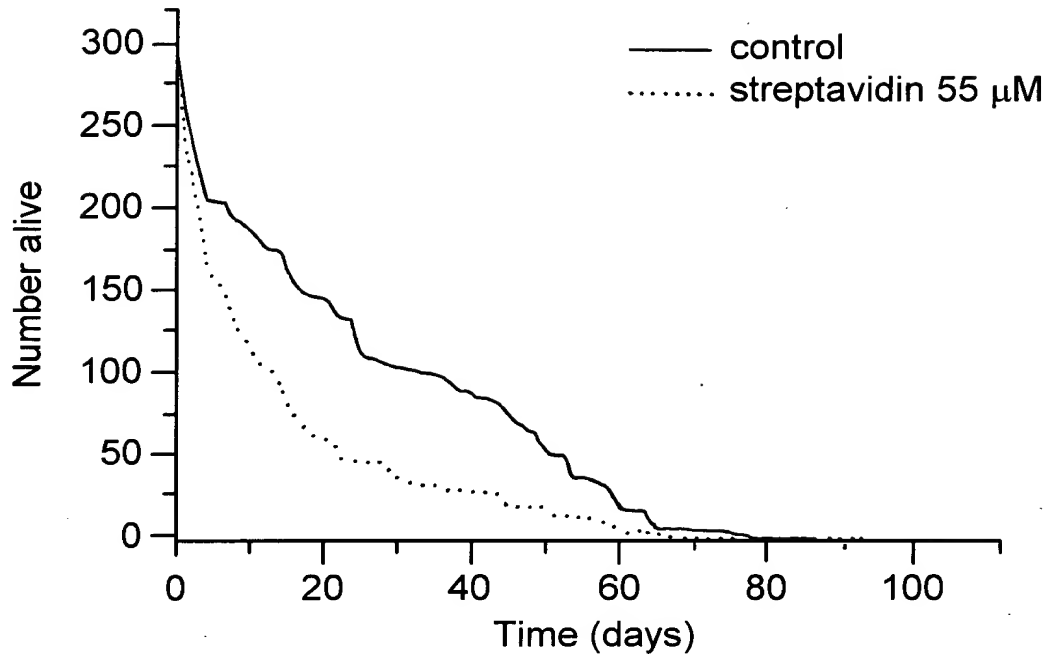


FIG. 38

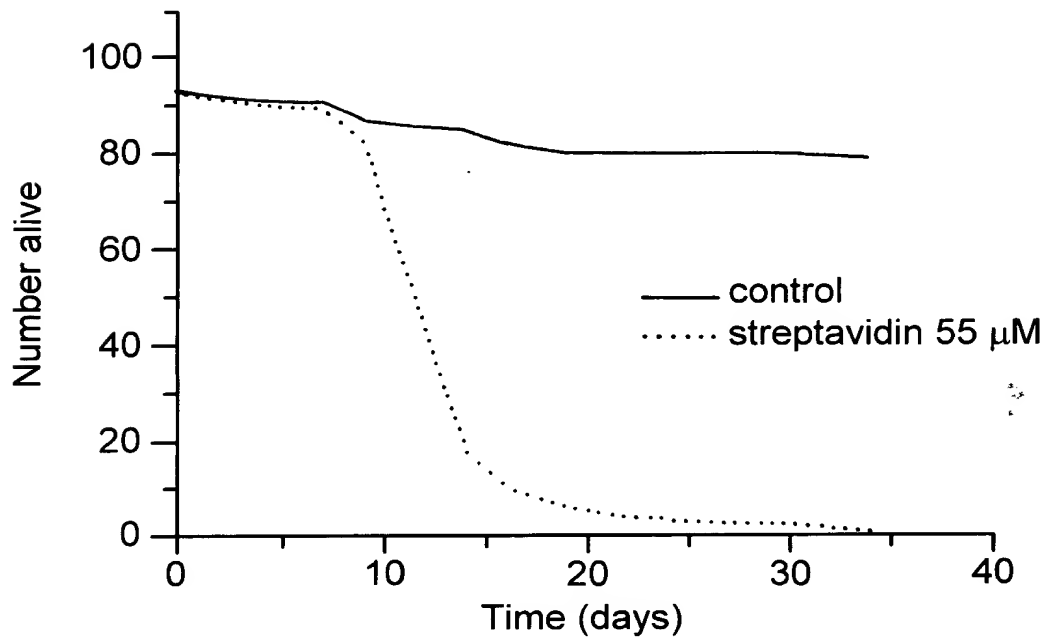


FIG. 39



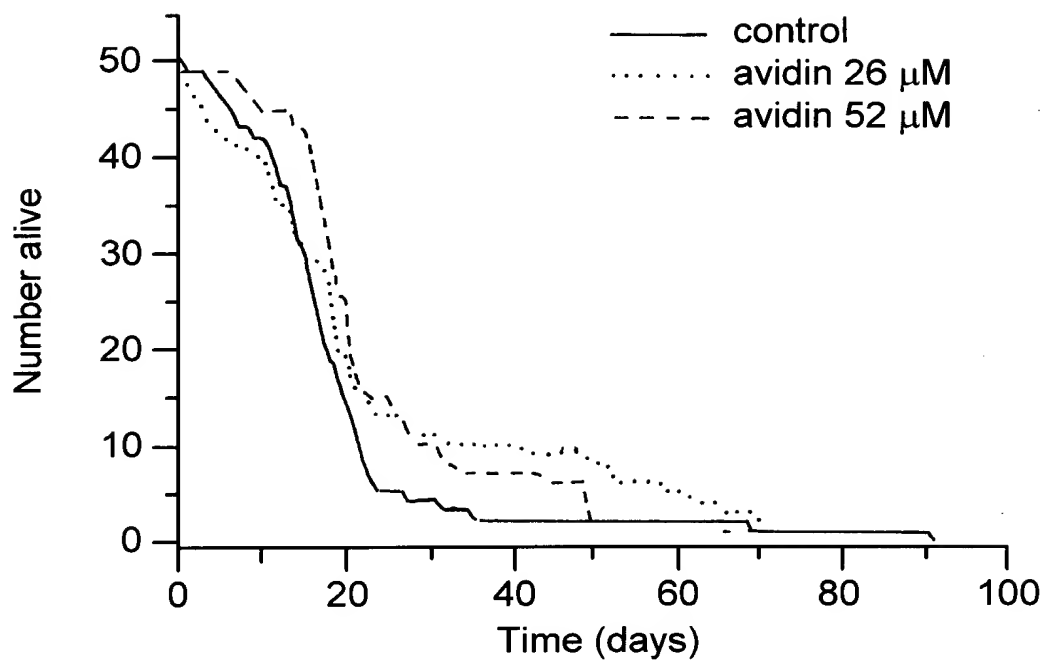


FIG. 40

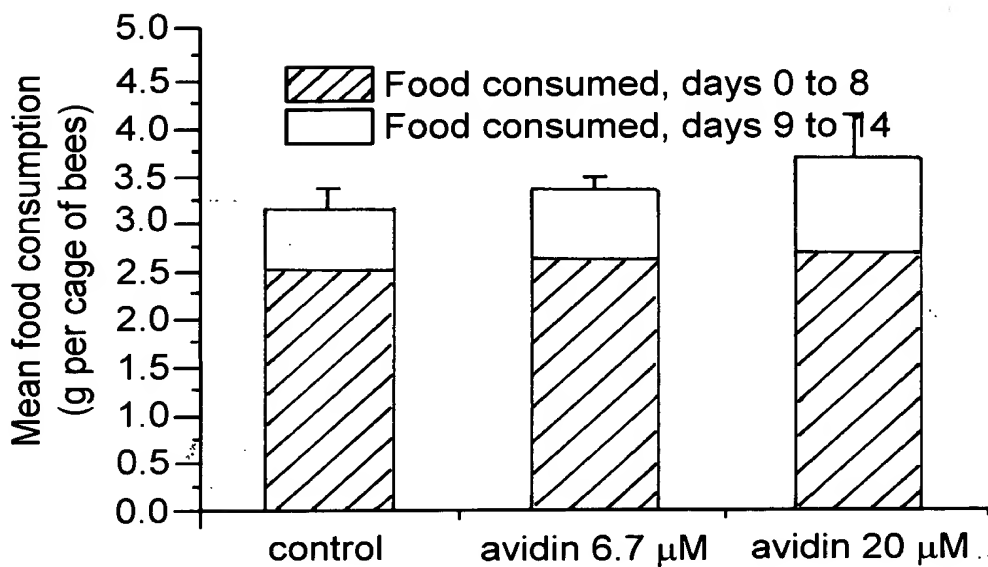


FIG. 41

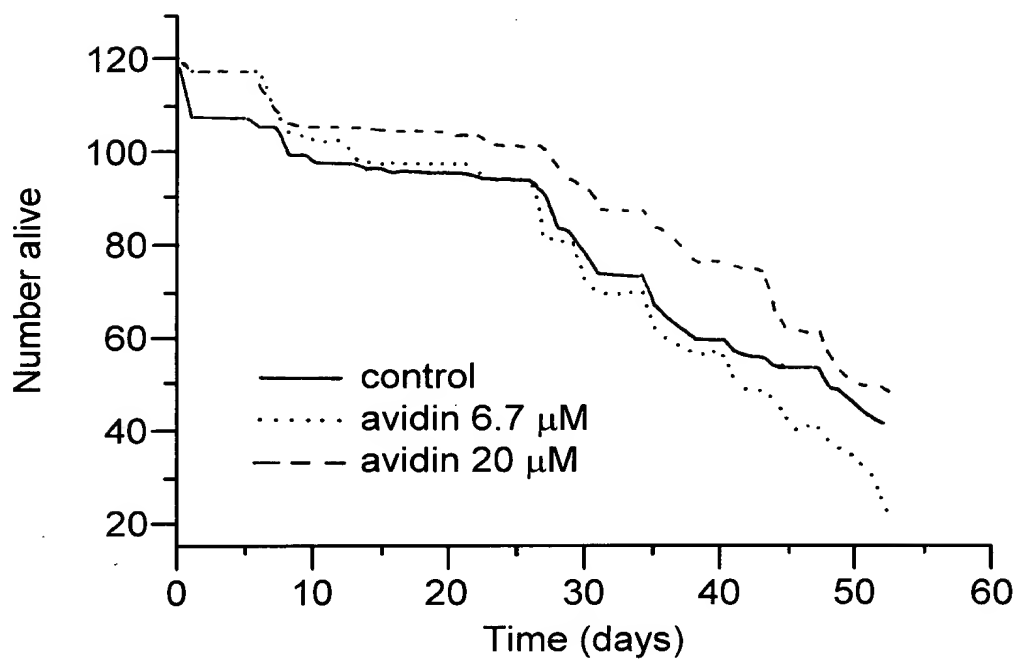


FIG. 42

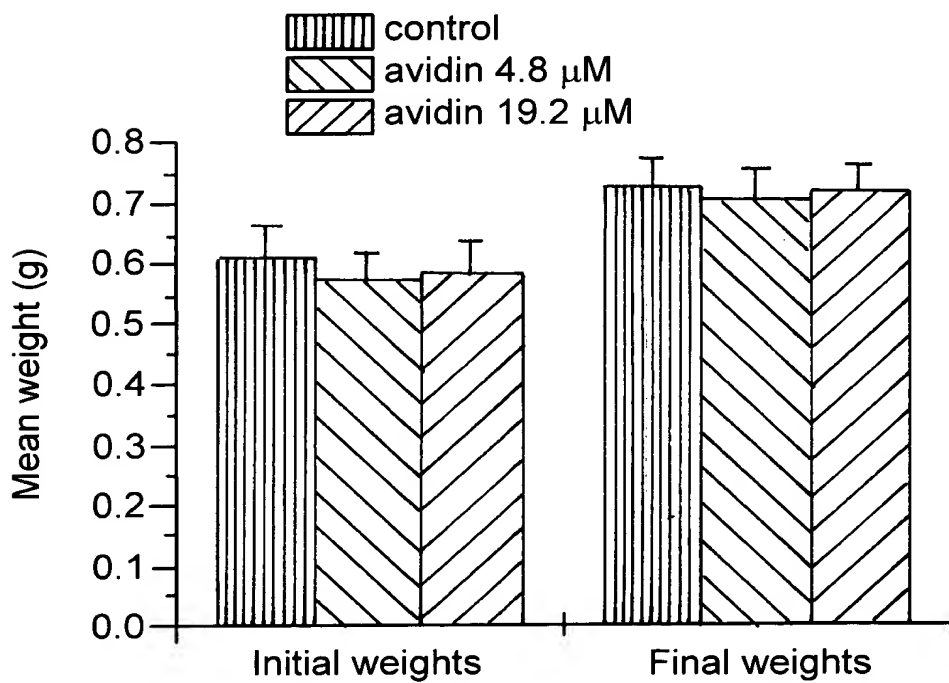


FIG. 43

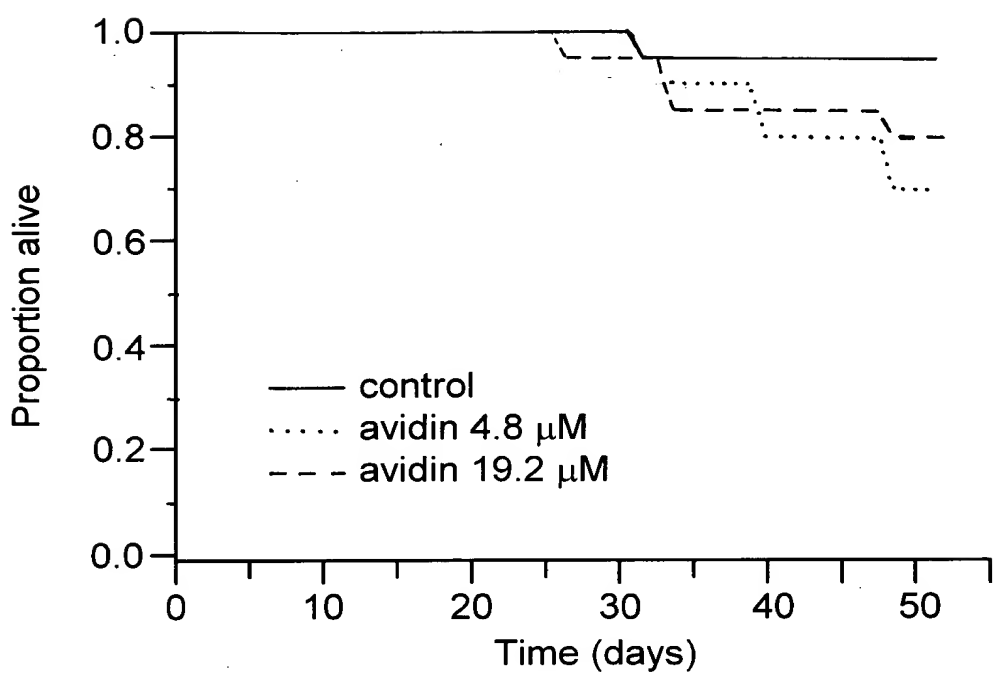


FIG. 44

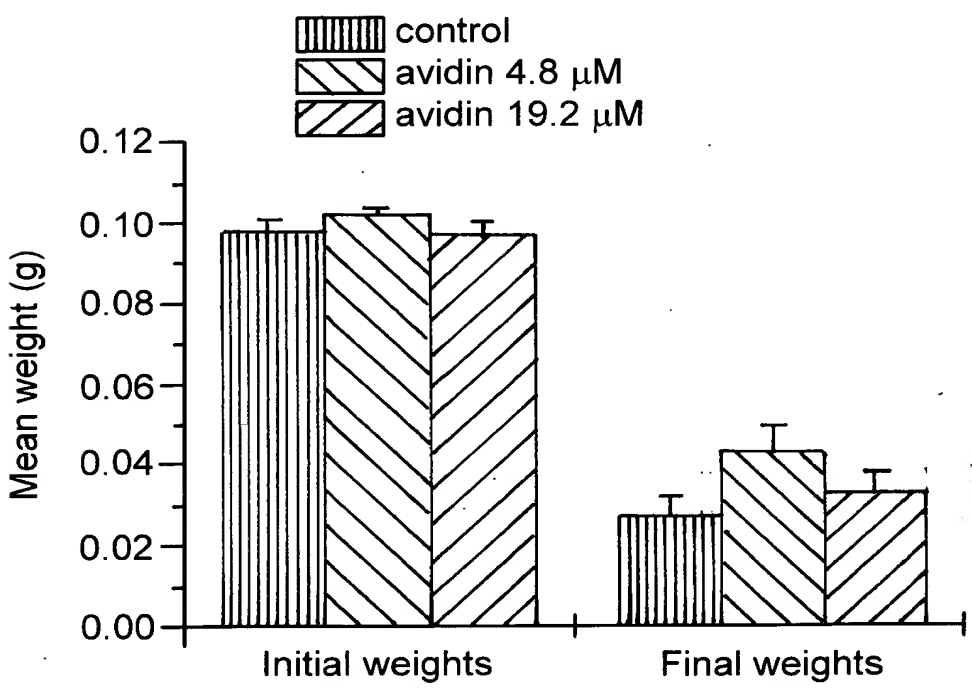


FIG. 45



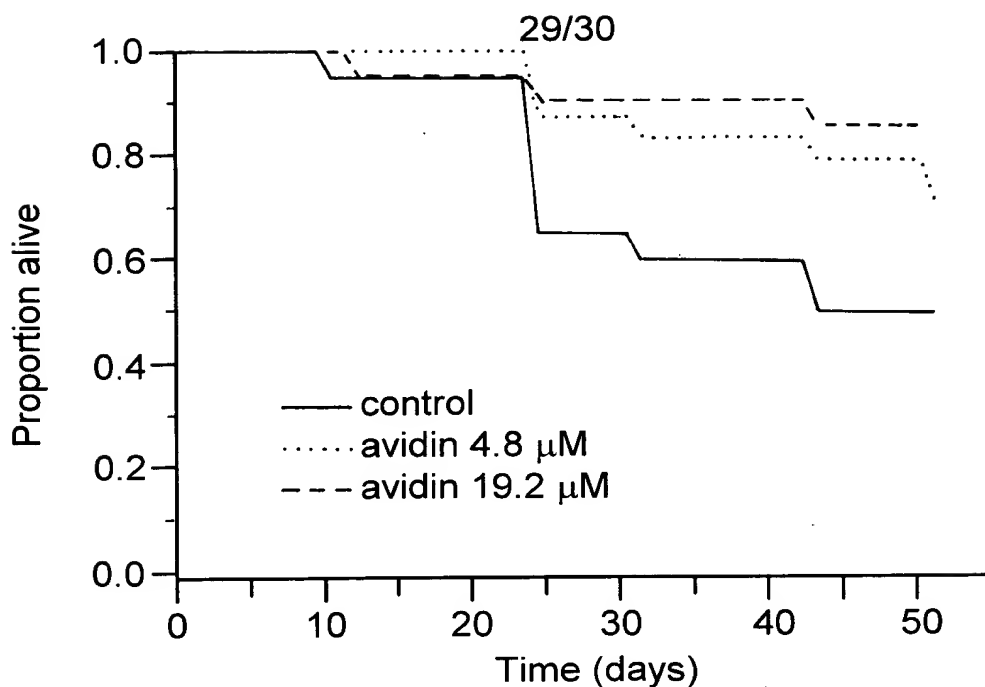


FIG. 46

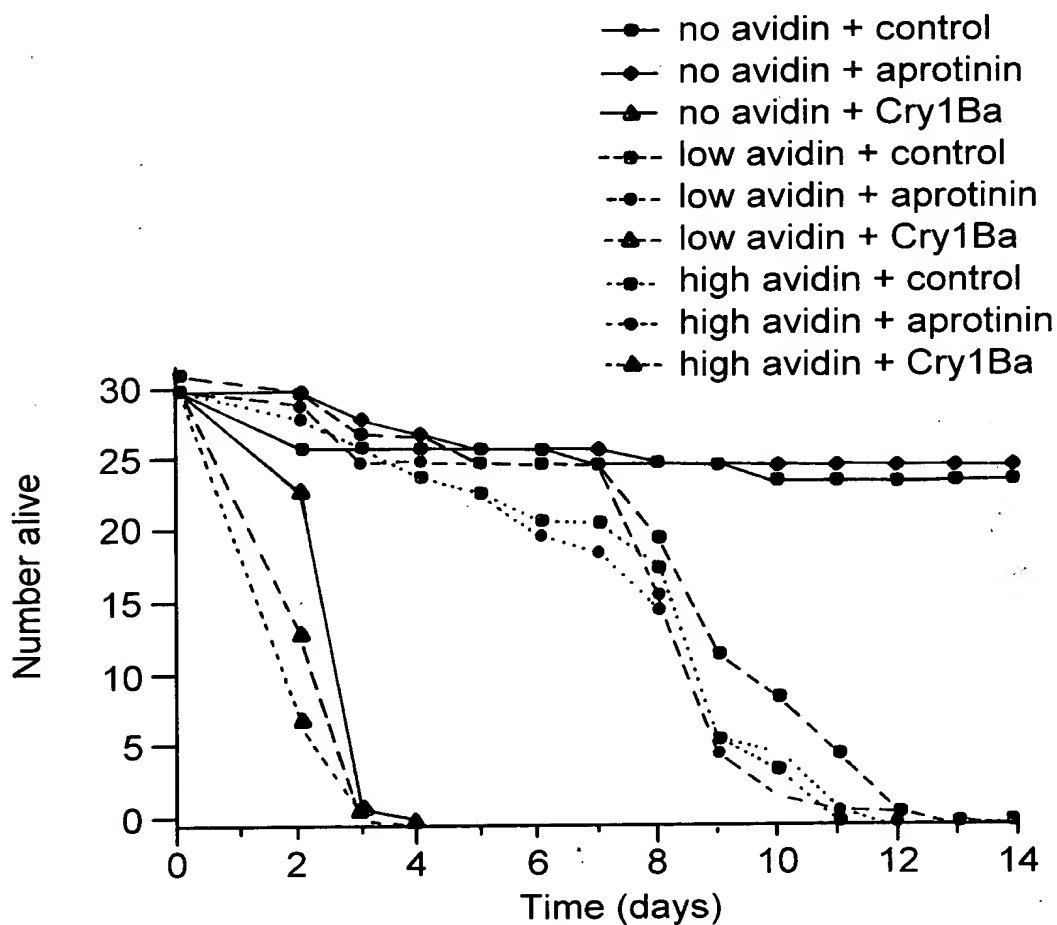


FIG. 47



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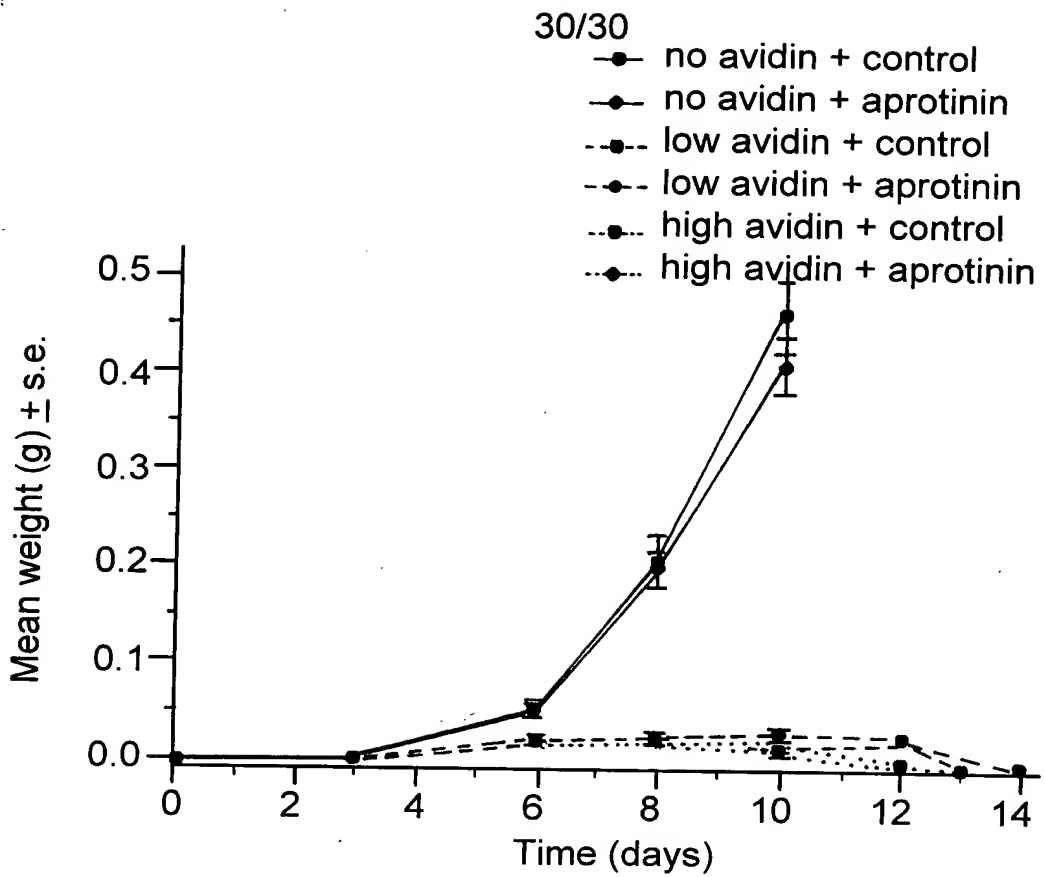


FIG. 48

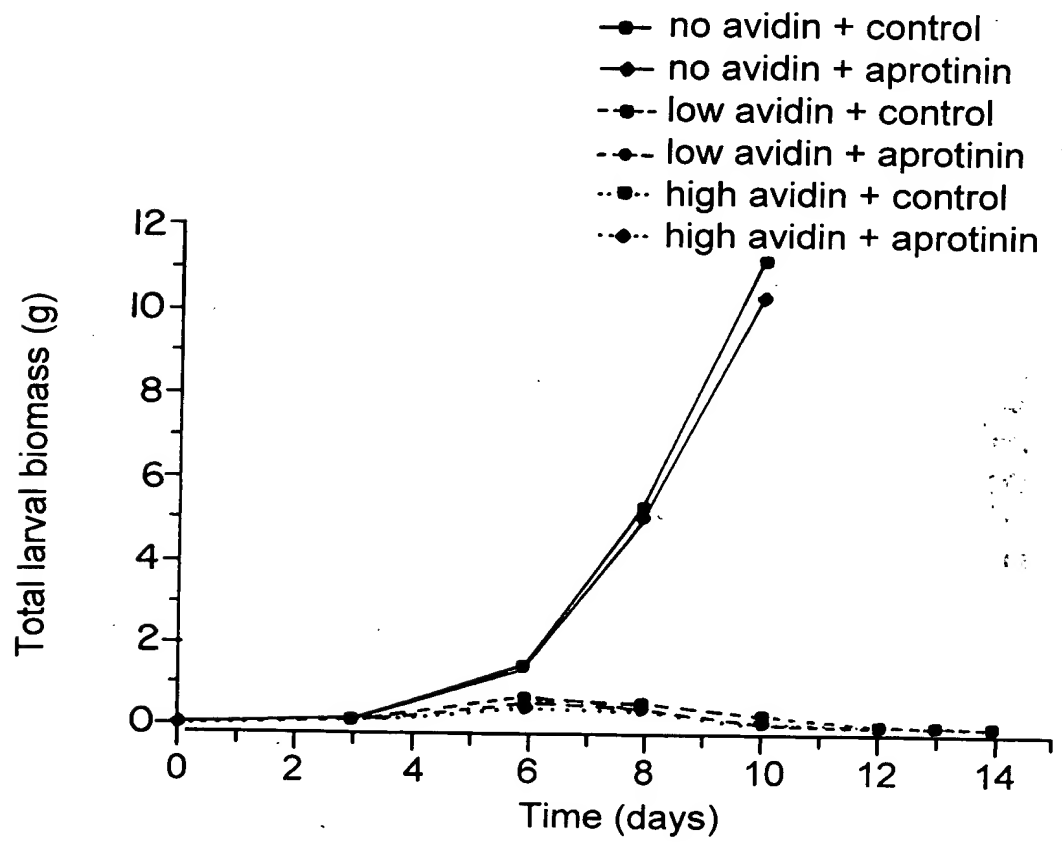


FIG. 49

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